

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 1, 2002, 21:19:11 ; Search time 21 Seconds
(without alignments)
1803.665 Million cell updates/sec

Title: US-09-732-597-2

Perfect score: 2062
Sequence: 1 MALKNFQCKNHPAPAKS.....KKAEHPVSFMSIFNRELEKI 394

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 segs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1545.5	75.0	385	2	A47245 acyl-[acyl-carrier
2	1490	72.3	396	1	OHCSAD acyl-[acyl-carrier
3	1422.5	69.0	411	2	T07806 acyl-[acyl-carrier
4	1410.5	68.4	399	1	OHSPAD acyl-[acyl-carrier
5	1408	68.3	396	2	B39170 acyl-[acyl-carrier
6	1406	68.2	396	1	A39173 acyl-[acyl-carrier
7	1396	67.7	398	2	S23351 acyl-[acyl-carrier
8	1395	67.7	396	2	T14264 acyl-[acyl-carrier
9	1386.5	67.2	393	2	S44202 acyl-[acyl-carrier
10	1386.5	67.2	399	2	S24995 acyl-[acyl-carrier
11	1385.5	67.2	393	2	T07633 acyl-[acyl-carrier
12	1381.5	67.0	401	2	EB4869 acyl-[acyl-ACP desat
13	1381	67.0	396	2	T14268 acyl-[acyl-carrier
14	1375.5	66.7	397	2	T10793 acyl-[acyl-carrier
15	1352	65.6	396	2	T14172 acyl-[acyl-carrier
16	1347.5	65.3	407	2	S71264 acyl-[acyl-carrier
17	1320.5	64.0	394	2	T51494 acyl-[acyl-carrier
18	1310.5	63.6	396	2	T04097 acyl-[acyl-carrier
19	1246	60.4	396	2	S31959 acyl-[acyl-carrier
20	1223.5	59.3	401	2	T51493 acyl-[acyl-carrier
21	1197	58.1	374	2	A96502 acyl-[acyl-carrier
22	295	14.3	328	2	T35035 probable acyl-[acyl
23	271.5	13.2	338	2	DB182 acyl-[ACP] desatur
24	256.5	12.4	338	2	H70810 probable desat pro
25	135	6.5	275	2	C87153 acyl-[ACP] desatur
26	122.5	5.9	2269	2	T28677 rhogly protein -
27	121.5	5.9	275	2	D70896 probable desat pro
28	114.5	5.6	1557	2	T18412 lipid-binding prote
29	108	5.2	616	2	A64341 hypothetical prote

30	105.5	5.1	393	2	C71836 tryptophan synthas
31	105.5	5.1	520	2	F90596 restriction-modifi
32	105.5	5.1	520	2	A99566 restriction-modifi
33	105.5	5.1	684	2	AE2004 hypothetical prote
34	104.5	5.1	524	2	T43050 cyclin E - Caenorh
35	104.5	5.1	570	2	T30156 hypothetical prote
36	103	5.0	244	2	C89811 hypothetical prote
37	102.5	5.0	393	2	F64679 tryptophan synthas
38	102.5	5.0	520	2	S49395 HsdM1 protein - My
39	101.5	4.9	846	2	JC7720 acetyltransferase
40	100.5	4.9	1027	2	T46296 hypothetical prote
41	100.5	4.9	3643	2	T36410 probable polyketid
42	100	4.8	604	2	T19682 hypothetical prote
43	99.5	4.8	517	2	T48283 ankryin-like prote
44	99.5	4.8	1120	2	JC7765 mitotic spindle as
45	99	4.8	782	2	A82940 hypothetical prote

ALIGNMENTS

RESULT 1

A47245
N:Alternate names: type II acyl-ACP desaturase
C:Species: Coriandrum sativum (coriander)
C>Date: 21-Jan-1994 #sequence_rev18-Nov-1994 #text_change 03-Jun-2002
C:Accession: A47245
R:Cañon, E.B.; Shanklin, J.; Ohlrogge, J.B.
Proc. Natl. Acad. Sci. U.S.A. 89, 11184-11188, 1992
A:Title: Expression of a coriander desaturase results in petroselinic acid production
A:Reference number: A47245; M0ID:93087491; PMID:1454797
A:Accession: A47245
A>Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-385 <CAH>
A:Cross-references: GB:M93115; NID:q167388; PIDN:AAC63059.1; PID:q167389
A>Note: sequence extracted from NCBI backbone (NCBIN:119750, NCBI:P.119751)
C:Superfamily: acyl-[acyl-carrier-protein] desaturase
C:Keywords: chloroplast; oxidoreductase

Query Match	Best Local Similarity	Score	Length	DB 2:	Length	DB 3:	Length	DB 4:	Length
Matches	296;	Conservative	42;	Mismatches	36;	Indels	31;	Gaps	5;
QY	1	MALKIN----	FOCKKNHPAPAKSPLPVRVSSP-----	RPFMASTVNSNVLDNLK	49				
DB	1	MALKNALMTLQCKRN-----	MTKRIAPQAGRVSKVSMASSTLASPLVFKLK	51					
QY	50	SPNQLQVTHSMPOKLEIFKSLDMDARNVLIHLKSVKSMOPDYLPDPVSDGFEEQVR	109						
DB	52	AG-----	REVDELFLNLSGWARDNLIHLKSVENSMOPDYLPDPVSDGFEEQVR	102					
QY	110	ELBRKEIPDDYFVVLVGMITEALPTYSMLNRCDGKIDETGAPSAWAMKTRAWTA	169						
DB	103	EMERKAKDIDFEEFVVLVGMITEALPTYSMLNRCDGKIDETGAPSAWAMKTRAWTA	162						
QY	170	EENRHGDLNKVLYLSGRVVRMKTEKTOYLIGSGMTEKNSYGFITTSOERATFI	229						
DB	163	EENRHGDLNKVLYLSGRVVRMKTEKTOYLIGSGMTEKNSYGFITTSOERATFI	222						
QY	230	SHANTAKLAOHYGDKNLAHICGSIASDEKRRATYATKIVKLAIEDDTVIAFADMRK	289						
DB	223	SHANTAKLAOHYGDKNLAHICGSIASDEKRRATYATKIVKLAIEDDTVIAFADMRK	282						
QY	290	KITMPAHLMTDGSDELLEFKHFTVAORVXYVALDYCDLLEFLVDKRVNERTGLSDEGR	349						
DB	283	KITMPAHLMTDGSDELLEFKHFTVAORVXYVALDYCDLLEFLVDKRVNERTGLSDEGR	342						
QY	350	KAOEYVCELGPKIRVVEKVOGKEKKKAHPVSFMSIFNRELEKI	394						
DB	343	KAOEYVCELGPKIRVVEKVOGKE--KKAVLPVAFSIFNRELEKI	385						

RESULT 2

OHSAD

acyl-[acyl-carrier-protein] desaturase (EC 1.14.19.2) precursor - castor bean
 N:Alternate names: stearyl-[acyl-carrier-protein] desaturase
 C:Species: Ricinus communis (castor bean)
 C>Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 03-Jun-2002
 C/Accession: S16463; A39170

R:Knutzon, D.S.; Scherer, D.E.; Schreckengost, W.E.
 Plant Physiol. 96, 344-345, 1991
 A:Title: Nucleotide sequence of a complementary DNA clone encoding stearyl-acyl carrier
 A:Reference number: S16463
 A:Accession: S16463

A:Molecule type: mRNA
 A:Residues: 1-396 <KNV>
 A:Cross-references: EMBL:X56508; NID:g21092; PIDN:CAA39859.1; PID:g21093
 R:Shanklin, J.; Somerville, C.
 Proc. Natl. Acad. Sci. U.S.A. 88, 2510-2514, 1991
 A:Title: Stearyl-acyl-carrier-protein desaturase from higher plants is structurally uni

A:Reference number: A39170; MUID:91172837; PMID:2006187
 A:Accession: A39170
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-396 <SHA>
 A:Cross-references: GB:M59858

A>Note: Parts of this sequence were confirmed by peptide sequencing
 C:Superfamily: acyl-[acyl-carrier-protein] desaturase
 C:Keywords: chloroplast; fatty acid biosynthesis; oxidoreductase
 F:1-33/Domain: transit peptide (chloroplast) #status predicted <TNP>
 F:34-396/Product: acyl-[acyl-carrier-protein] desaturase #status predicted <MAT>

Query Match Best Local Similarity 72.3%; Score 1490; DB 1; Length 396;
 Matches 286; Conservative 50; Mismatches 52; Indels 14; Gaps 5;

OY 1 MALKLN-FQCKKNHFAFAKSPLEVTFRVSSPRVMASTVNSNVLDNLKSP-----PN 53
 Db 1 MALKLNFLSQTOQKLPFALPMASTR--SPKFTMASTLSSGSEVENLKPPMPREHV 58
 OY 54 LQYTHSPPOKLEIFKSLDWMARNVLIHLKSVKSWOPDYLDPVSDGFEQVRELE 113
 Db 59 VQYTHSPPOKLEIFKSLDWMARNVLIHLKSVKSWOPDYLDPVSDGFEQVRELE 118
 OY 114 RAKEIPDDYFVVLVGMITTEALPTYMSMLNRCDGIDETGAEFSANAMTTRAVTAENR 173
 Db 119 RAKEIPDDYFVVLVGMITTEALPTYMSMLNRCDGIDETGAEFSANAMTTRAVTAENR 178
 OY 174 HGDLNKKYLYSGRVDMRKTEKTIOYLIGSGMDIKSENSPYLGPIYTSFOERATFISHAN 233
 Db 179 HGDLNKKYLYSGRVDMRKTEKTIOYLIGSGMDIKSENSPYLGPIYTSFOERATFISHAN 238
 OY 234 TAKLAQHYGDKNLAHICGSIASDEKRNHATYTKIVEKLAIEDPTTVIAFADMKRKITM 293
 Db 239 TAKLAQHYGDKNLAHICGSIASDEKRNHATYTKIVEKLAIEDPTTVIAFADMKRKITM 298
 OY 294 PAHLMTDGSDELFFKHETVAORVXYXSALDYCDLIEFLVDKNNVERLTGLSEGRKAQF 353
 Db 299 PAHLMTDGSDELFFKHETVAORVXYXSALDYCDLIEFLVDKNNVERLTGLSEGRKAQF 358
 OY 354 YVCELGPKIRVEEKYQKREKKRAEHP--VSFSWIFNRELKI 394
 Db 359 YVCELGPKIRVEEKYQKREKKRAEHP--VSFSWIFNRELKI 394

RESULT 3

T07806

acyl-[acyl-carrier-protein] desaturase (EC 1.14.19.2) precursor - soybean
 N:Alternate names: stearyl-acyl carrier protein desaturase
 C:Species: Glycine max (soybean)
 C>Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 03-Jun-2002
 C/Accession: T07806

R:Chen, B.Y.; Janes, H.W.
 submitted to the EMBL Data Library, July 1994

A:Reference number: 216145

A:Accession: T07806

A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-411 <CHE>

A:Cross-references: EMBL:L34346; NID:g508602; PIDN:AAA92462.1; PID:g508603
 C:Genetics:
 A:Gene: SACP
 A:Genome: nuclear

C:Superfamily: acyl-[acyl-carrier-protein] desaturase
 C:Keywords: chloroplast; oxidoreductase
 F:1-29/Domain: transit peptide (chloroplast) #status predicted <TNP>

Query Match Best Local Similarity 69.0%; Score 1422.5; DB 2; Length 411;
 Matches 274; Conservative 46; Mismatches 54; Indels 31; Gaps 4;

OY 1 MALKLNFOCKKNHFAFAKSPLEVTFRVSSPRVMASTVNSNVLDNLKSP- 51
 Db 1 MALKLN-----PIPTQFSLPQMASLRSPFRMASTRSGSEVENIKKPF 46
 OY 52 -----PNQYTHSPPOKLEIFKSLDWMARNVLIHLKSVKSWOPDYLDPVSDGFE 106
 Db 47 TPPEVHVQYTHSPPOKLEIFQSLDWMARNVLIHLKSVKSWOPDYLDPVSDGFE 106
 OY 107 QVRELERAKEIPDDYFVVLVGMITTEALPTYMSMLNRCDGIDETGAEFSANAMTTRA 166
 Db 107 QVRELERAKEIPDDYFVVLVGMITTEALPTYMSMLNRCDGIDETGAEFSANAMTTRA 166
 OY 167 WTAEENRHGDLNKKYLYSGRVDMRKTEKTIOYLIGSGMDIKSENSPYLGPIYTSFOERA 226
 Db 167 WTAEENRHGDLNKKYLYSGRVDMRKTEKTIOYLIGSGMDIKSENSPYLGPIYTSFOERA 226
 OY 227 TFIHANTAKAQHYGDKNLAHICGSIASDEKRNHATYTKIVEKLAIEDPTTVIAFAD 286
 Db 227 TFIHANTAKAQHYGDKNLAHICGSIASDEKRNHATYTKIVEKLAIEDPTTVIAFAD 286
 OY 287 MRKTIAPAHLMYDGSDELFFKHETVAORVXYXSALDYCDLIEFLVDKNNVERLTGLSD 346
 Db 287 MRKTIAPAHLMYDGSDELFFKHETVAORVXYXSALDYCDLIEFLVDKNNVERLTGLSD 346
 OY 347 EGKRAQEVCELGPKIRVEEKYQKREKKRAEHPVSFSWIFNRE 391
 Db 347 EGKRAQEVCELGPKIRVEEKYQKREKKRAEHPVSFSWIFNRE 391

RESULT 4

OHSAD

acyl-[acyl-carrier-protein] desaturase (EC 1.14.19.2) precursor - spinach
 N:Alternate names: stearyl-acyl-carrier-protein desaturase
 C:Species: Spinacia oleracea (spinach)
 C>Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 03-Jun-2002
 C/Accession: S22480; S18183

R:Nishida, I.; Beppu, T.; Murata, N.
 Plant Mol. Biol. 19, 711-713, 1992
 A:Title: Nucleotide sequence of a cDNA clone encoding a precursor to stearyl-acyl-c

A:Reference number: S22480; MUID:92329733; PMID:1627785
 A:Accession: S22480

A:Molecule type: mRNA
 A:Residues: 1-399 <NTS>

A:Cross-references: EMBL:X62898; NID:g21229; PIDN:CAA44687.1; PID:g21230
 C:Superfamily: acyl-[acyl-carrier-protein] desaturase
 C:Keywords: chloroplast; fatty acid biosynthesis; oxidoreductase
 F:1-35/Domain: transit peptide (chloroplast) #status predicted <TNP>
 F:36-399/Product: acyl-[acyl-carrier-protein] desaturase #status predicted <MAT>

Query Match Best Local Similarity 68.4%; Score 1410.5; DB 1; Length 399;
 Matches 273; Conservative 59; Mismatches 55; Indels 19; Gaps 8;

OY 1 MALKLN-----FQCKKNHFAFAKSPLEVTFRVSSPRVMASTVNSN-VYLDNLK--SP 51
 Db 1 MALKLNVPSTPOCKR--LPFSFSPROTSPRR--SPKFTMASTLSSSSPKAESTLKKPFSP 56

QY	52	P - NLOVTHSMPOKEIKFSLSDMARNVNIHLKSVKSKSQDDLYLPPVSDSEFEQY	108
		::::: ::::: ::::: ::::: ::::: :::::	
Db	57	PREVHYVTHSMFOEKETIEFKSLSEGAEEENLVHLKPEVKCQOPDLYLPDPAISEDFEROY	116
QY	109	RELREARKEITPDYFVYLVADMTEBEPALPTYSMLRRCGIDKEFGAEPASAAMMTRAMT	168
Db	117	KEIOERAKEITPDLYVLYVADMTEBEPALPTYQTMNTLDGAKDEFGASTSAWVTRAMT	176
QY	169	AEENRHDDLNTKLYLVSGRVDMRIEKTQYLLGSGMDIKSENSPYLGEIYVSFOERATF	228
Db	177	AEEHRHDDLNTKLYLVSGRVDMRIEKTQYLLGSGMDIRTENNPYLGEIYVTSFOERATF	236
QY	229	ISHANTAKLQHYGDKNLAHIGSIASDEKRNATATYKIVEKLAETIDPTVIYAFADMKR	288
Db	237	VSHNSARLKEHGDJLMAOICGIIASDEKRHEATTATYKIVEKLEFIDPATVIYAFADMMK	296
QY	289	KKIMPAHLWYDSDDELFFHFTPAVQORXYVSALDYCILEFLVDKNWVEVLTLSDEG	348
Db	297	KKISMPAHLWYDGDGDLLEPHFSAVQORXYVYAKYADILEFLVGRWVEVLTLSDEG	356
QY	349	RKAQYVCCELPKIRIYVEEVQOKEKKKKAEPHVSPTJFNRELKI 394	
Db	357	OKADQYVCSPKIRIRLEER--AREAKQAP-SMPSWJLFDQOVU 399	

RESULT 5
B39170
acyl-[acyl-carrier-protein] desaturase (EC 1.14.19.2) precursor - cucumber
C:Species: Cucumis sativus (cucumber)
C:Date: 24-Jan-1992 #sequence,revision 24-Jan-1992 #text-change 03-Jun-2002
C:Accession: B39170
R:Shanklin, J.; Somerville, C.
Proc. Natl. Acad. Sci. U.S.A. 88, 2510-2514, 1991
A:Title: Stearoyl-acyl-carrier-protein desaturase from higher plants is structurally un
A:Reference number: A39170; M01D:91172837; PMID:2006187
A:Accession: B39170
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-396 <SHA>
A:Cross-references: GB:M59857
C:Superfamily: acyl-[acyl-carrier-protein] desaturase
C:Keywords: chloroplast; oxidoreductase

[illegible]

```
Db      354 QKADYVICALPARIRKLEERAQGRAK---EGPTIPFSWIFDRQVKL 396
```

RESULT 6

acyl-[acyl-carrier-protein] desaturase (BC 1.14.19.2) precursor - safflower
C:Species: Carthamus tinctorius (safflower);
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 03-Jun-2002
C:Accession: A39173
R:Thompson, G.A.; Scherer, D.E.; Foxall-Van Aken, S.; Kenny, J.W.; Young, H.L.; Shultz
Proc. Natl. Acad. Sci. U.S.A. 88, 2578-2582, 1991
A:Title: Primary structures of the precursor and mature forms of stearoyl-acyl carrier
A:Reference number: A39173, MUID:91172850, PMID:2006194
A:Accession: A39173
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-396 <RHO>
A:Cross-references: GB:661109; NID:g167196; PIND:AAA33021.1; PID:g167197
C:Superfamily: acyl-[acyl-carrier-protein] desaturase
C:Keywords: chloroplast; oxidoreductase

Query Match	68.2%	Score 1406	DB 1	Length 396
Best Local Similarity	67.1%	Pred. No. 4.2e-95		
Matches 271	Conservative 54	Mismatches 61	Indels 18	Gaps 5

QY	1	MALKI----	NEPQCKNHHPAFKSP	LPTVRVSSP	PRFMASTVNSMVL	DNLKSP-----	51				
Db	1	MALRTPPT	LTLOSERKRS	SPFK-----	ANLSPKFA	MASTIGSS	TPKVDNKKKRPQPRE	56			
QY	52	PNLOVTHSP	PROKLEIFKSL	DDMARNNVL	HLKSVKSMO	PODYLP	PDVSDGFEEQYREL	111			
Db	57	VHVQVTHSP	PROKLEIFKSI	EGMAEQNL	ITVHLK	PVEKCMQ	QODFLP	DPASBGDFEQYEL	116		
QY	112	REKAKEIPDDY	FVVLVCGMTE	EALPTVMSLN	KRCDG	IKDETGA	BPSSMAMMTAA	TAEE	171		
Db	117	RARAKEIPDDY	FVVLVCGMTE	EALPTVQTM	LNFLDGR	DTGASL	TPWAWTATMA	TAEE	176		
QY	172	NRHGDLKKY	LYLUSGRVDM	RKTEKTIQV	LLISGMD	IKENS	PRYIGFYT	TSQERATF	231		
Db	177	NRHGDLTTY	LYLUSGRVDM	ROIQTKI	QVLLISG	MDPR	ENSPYIGFYT	TSQERATF	236		
QY	232	ANTAKLAOH	YDGKMLNHL	ICGSIAS	DEKRNHATAY	KRYEKL	ELIDPDTV	VIAFADMR	291		
Db	237	GNTARH	ANDHGDV	KLQICG	ITASEK	RHNPTAY	KRYEKL	ELIDPDTV	LAFADMR	296	
QY	292	TPRAHLM	YDGSDEL	LFKHFT	VVAQR	VXYV	SALDYCD	LEPLVDK	MNVERLT	351	
Db	297	SMRAHLM	YDGRDDN	LFEHFS	AVAOR	LGVYTA	KDVA	DILEPLV	CGRMK	356	
QY	352	QEVYCE	LGPKTR	RVEEK	YQGEK	KKKA	EHN- VSPSW	IFNR	ELKI	394	
Db	357	QDVYCG	LPRLR	RLRE	AOGR	AK-----	EGV	PP	PSW	IFN	396

RESULT 7

acyl-[acyl-carrier-protein] desaturase (EC 1.14.19.2) precursor - turnip
C:Species: Brassica rapa (turnip)
C:Date: 22-Nov-1993 #sequence,revision 10-Nov-1995 #text,change 03-Jun-2002
C:Accession: S23351
R:Knutzon, D.S.; Thompson, G.A.; Radke, S.E.; Johnson, W.B.; Knauf, V.C.; Kridl, J.C.
Proc. Natl. Acad. Sci. U.S.A. 89, 2624-2628, 1992
A:Title: Modification of Brassica seed oil by acyltransferase expression of a stearyl-acyl
A:Reference number: S23351; MUID:92212881; PMID:1557366
A:Accession: S23351
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-398 <KNU>
A:Cross-references: EMBL:X60978; MID:g17928; PIDN:CAA3294.1; PID:g17929
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1991
C:Superfamily: acyl-[acyl-carrier-protein] desaturase
:Keywords: chloroplast; oxidoreductase

acyl-[acyl-carrier-protein] desaturase (EC 1.14.19.2) precursor - Commerson's wild po

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182  LLHQLYLSGSRVDKROQLQKTIQYLIGSGMDPRHNSPGLFITTSQEQATPFLSHGRT 241
      |||||.....:|||||.....:|||||.....:|||||.....:|||||.....:
QY  237  LAQHYGKNLAHIGSIIASDEKRNHATVYTVKELADIDPDTVIAFADMMRRKKTTPAH 296
      ||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  242  HAKYGDGLKLAQICGTIAADEKRNHETAYTKIAKLEIIDBDGTVALFADMMRRKKTSMRN 301
      |||||.....:|||||.....:|||||.....:|||||.....:|||||.....:
QY  297  LMYGSDLELFKFTTAVARVXYSSALDYCDLLEFLYDGMNVRERLGLSDEGRKAQEVYC 356
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  302  LMYGRDDLEDFHFSAAQRLGYTTAKDIADLLEFLYGVGRKKAADLTGLSGEGRKAQDYVC 361
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY  357  ELGPKIRVEKAVQGEKKRKAHP-VSPSWLFRNBLKI 394
      | : ||| ||| : | : ||||| ||| : ||||| ||| : ||||| ||| : |||||
Db  362  GLPSRIRLEREAARAK----EGPSIPSWLFRNRYKL 396
      |||||.....:|||||.....:|||||.....:|||||.....:|||||.....:

RESULT 9
S44202
acyl-[acyl-carrier-protein] desaturase (EC 1.14.19.2) precursor - Commerson's wild po
N:Alternate names: stearyl-ACP desaturase
C:Species: Solanum commersonii (Commerson's wild potato)
C:date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 03-Jun-2002
C:accession: S44202
R:Trucci, M.; Grillo, S.; Costa, A.; Leone, A.
Submitted to the EMBL Data Library, April 1994
A:Reference number: S44202
A:Accession: S44202
A:Molecule type: mRNA
A:Residues: 1-393 <TRU>
C:cross-references: EMBL:X78935; NID:g474832; PIDN:CAA55535.1; PID:g474833
C:genetics:
A:genome: nuclear
C:superfamily: acyl-[acyl-carrier-protein] desaturase
C:keywords: chloroplast; fatty acid biosynthesis; oxidoreductase
F:1-30/Domain: transit peptide (chloroplast) #status predicted <TNP>
F:31-993/Product: acyl-[acyl-carrier-protein] desaturase #status predicted <MAT>

Query Match 67.2%; Score 1386.5; DB 2; Length 393;
Best Local Similarity 66.3%; Pred. No. 1.1e-93;
Matches 267; Conservative 53; Mismatches 64; Indels 19; Gaps 5;

QY 1 MALKLN---EQCKKHNRPAFAKSPLEPTRVSSPRVFAASTVNSNMYLNLK---SPR-- 52
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 MALNFSPTFOSIKT-----TRRPCSPILKSPRVFMASTLRPSYEDGVNKKRPFSPRE 53
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 53 -NLQVTHSMSPQKLEIFKSLDDMARNNVLIHKVEKSWQPDVLPVPSIDGSEBOYREL 111
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 54 VHVQVTHSMPEKREIRFELSILGWADNNILGLKVEKQWASDFLPDPAEGEDYKEL 113
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 112 RPRKEATPDYFVVLVGMTTEBALPTYMSMLNRCDSIKDETGAERSAMAMTRAVTAEE 171
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 114 RERKEIPDDYFVVLVGMTTEBALPTYQTMLTLDVREDTGASLTPLMAIWRVMTADE 173
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 172 NRHGDLKKYULSGVDMRKIEKTIQYLIGSGMDIKSENSPLTGLFTYTSFQERATFISH 231
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 174 NRHODLNLKYLISGRVDMQIEKTIQYLIGSGMDPTENNPHLGLFTYSFQERATFISH 233
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 232 ANTKLAQHYGKNLAHIGSIIASDEKRNHATVYTVKELAEIDPDTVYIAFADMMRRKKT 291
      ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 234 GNTFRHAKHEHODMKLAQVCGIIAADEKRNHETAYTKIYKLEFVDPRGCTYLAADMMRRKKT 293
      ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
QY 292 TMRPHLWYDGSDELLEHFTAVARVXYSSALDYCDLLEFLYDGMNVRERLGLSDEGRKA 351
      : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 294 SMPRHLLWYDGDSDLLEHFTSTVAORLGVYTTAKDIADLLEFLYGVGRKKAADLTGLSGEGRKA 353
      : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
QY 352 QEVYVCELGPKIRVEEKVQGEKKRKAHPVSPSWLFRNBLKI 394
      : ||| : ||| : ||| : | : | : | : ||| : ||| : ||| : ||| : ||| :
Db 354 RDYVCGILAPRIKLEIRERAKARAKA---PVSPSWFGADIKL 393
      : ||| : ||| : ||| : | : | : | : ||| : ||| : ||| : ||| : ||| :

RESULT 10
S24955
acyl-[acyl-carrier-protein] desaturase (EC 1.14.19.2) precursor - Arabidops
```


[illegible]

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Db 1 MAMKLNALMTLQCPKRN-----MFTRIAPQAGRVRSKYSMASTLHASPLVFEDK 51
QY 50 SPNNLOVTHSNPPOKLEIFKSLDDMARNNVLIHKSVKSNQPODYLDPDVSDFGEEOVR 109
Db 52 AG-----RPEVDLEFNSLEGWARDNITLVHLKSVENSWQPODYLDPDTSDAFEDQVK 102
QY 110 ELERAKELIPDDYFVYLVGDMITEEALPTYSMLNRCDGIKDETGAEPSSAMAMTRAWTA 169
Db 103 EMERAKDIPDEFYVYLVGDMITEEALPTYSMLNRCDGIKDDTGAQPTSNATWTAWTA 162
QY 170 EENRHGDLNKKYLYLSGRVDMRKIEKTYLYLIGSGMDIKSENSPYLGFYTSFORAFETI 229
Db 163 EENRHGDLNKKYLYLSGRVDMRKIEKTYLYLIGSGMDTKENCYPMGFTYTSFORAFETI 222
QY 230 SHANTAKLAOHYGDKNLAHICGSIASDEKRAHATATYKIVEKLAIEDPTTYIAFADMMRK 289
Db 223 SHANTAKLAOHYGDKNLAHICGSIASDEKRAHATATYKIVEKLAIEDPTTYIAFADMMRK 282
QY 290 KITMPAHLMYDGSDELFRKHTAVARVYXSALDYCDILEFLVDKNVVERLTGSLDEGR 349
Db 283 KIOMPAHAMYDGSDDMLFKHFTAVSQOIGVYSAMDYCDILDFLVKNNVAKMTGLSGEGR 342
QY 350 KAOEYVCELGPKIRVEEKVQGEKKKAHEPVFSWIFNRLEKI 394
Db 343 KAOEYVCSLAAKIRVEEKVQGE--KRAVLPAFWSWIFNRROI 385

RESULT 2
US-08-329-560-4

Sequence 4, Application US/08329560
Patent No. 5654402
GENERAL INFORMATION:
APPLICANT: CAHOON, Edgar B.
TITLE OF INVENTION: Methods and Compositions Relating to
TITLE OF INVENTION: Plant 6-Delta Palmitoyl-Acyl Carrier Protein Desaturase
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pioneer Hi-Bred International, Inc.
STREET: 700 Capital Square, 400 Locust Street
CITY: Des Moines
STATE: Iowa
COUNTRY: US
ZIP: 50309
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/329,560
FILING DATE: 26-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Yates, Michael E.
REGISTRATION NUMBER: 36,063
REFERENCE/DOCKET NUMBER: 0284US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (515) 248-4800
TELEFAX: (515) 248-4844
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 385 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-329-560-4

Query Match 74.9%; Score 1544.5; DB 1; Length 385;
Best Local Similarity 73.1%; Pred. No. 2.2e-148;
Matches 296; Conservative 42; Mismatches 36; Indels 31; Gaps 5;
QY 1 MALKLN----FOCKKNHPAFAKSPLPVTRYSSP-----RVFASATYNSNSMWLDNLK 49

Db 1 MAMKLNALMTLQCPKRN-----MFTRIAPQAGRVRSKYSMASTLHASPLVFEDK 51
QY 50 SPNNLOVTHSNPPOKLEIFKSLDDMARNNVLIHKSVKSNQPODYLDPDVSDFGEEOVR 109
Db 52 AG-----RPEVDLEFNSLEGWARDNITLVHLKSVENSWQPODYLDPDTSDAFEDQVK 102
QY 110 ELERAKELIPDDYFVYLVGDMITEEALPTYSMLNRCDGIKDETGAEPSSAMAMTRAWTA 169
Db 103 EMERAKDIPDEFYVYLVGDMITEEALPTYSMLNRCDGIKDDTGAQPTSNATWTAWTA 162
QY 170 EENRHGDLNKKYLYLSGRVDMRKIEKTYLYLIGSGMDIKSENSPYLGFYTSFORAFETI 229
Db 163 EENRHGDLNKKYLYLSGRVDMRKIEKTYLYLIGSGMDTKENCYPMGFTYTSFORAFETI 222
QY 230 SHANTAKLAOHYGDKNLAHICGSIASDEKRAHATATYKIVEKLAIEDPTTYIAFADMMRK 289
Db 223 SHANTAKLAOHYGDKNLAHICGSIASDEKRAHATATYKIVEKLAIEDPTTYIAFADMMRK 282
QY 290 KITMPAHLMYDGSDELFRKHTAVARVYXSALDYCDILEFLVDKNVVERLTGSLDEGR 349
Db 283 KIOMPAHAMYDGSDDMLFKHFTAVSQOIGVYSAMDYCDILDFLVKNNVAKMTGLSGEGR 342
QY 350 KAOEYVCELGPKIRVEEKVQGEKKKAHEPVFSWIFNRLEKI 394
Db 343 KAOEYVCSLAAKIRVEEKVQGE--KRAVLPAFWSWIFNRROI 385

RESULT 3
US-08-539-798-3

Sequence 3, Application US/08539798
Patent No. 5614400
GENERAL INFORMATION:
APPLICANT: CAHOON, Edgar B.
TITLE OF INVENTION: Methods and Compositions Relating to
TITLE OF INVENTION: Plant 6-Delta Palmitoyl-Acyl Carrier Protein Desaturase
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pioneer Hi-Bred International, Inc.
STREET: 700 Capital Square, 400 Locust Street
CITY: Des Moines
STATE: Iowa
COUNTRY: US
ZIP: 50309
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/539,798
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/329,560
FILING DATE: 26-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Yates, Michael E.
REGISTRATION NUMBER: 36,063
REFERENCE/DOCKET NUMBER: 0284US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (515) 248-4800
TELEFAX: (515) 248-4844
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 396 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-539-798-3

Query Match 72.3%; Score 1490; DB 1; Length 396;

Best Local Similarity 71.1%; Pred. No. 8e-143;
Matches 286; Conservative 50; Mismatches 52; Indels 14; Gaps 5;

QY 1 MALKN-FCKKNNPAAFAKSPLEPVTVSSPRVPMASSTVNSMVLNDLKSP-----PN 53
1 MALKNFLSQTKLPSPALPMASTR--SPKFTMASTLKSCKSEVENLKKPFMPPREVH 58
Db 1 MALKNFLSQTKLPSPALPMASTR--SPKFTMASTLKSCKSEVENLKKPFMPPREVH 58

QY 54 LQVTHSPPOKLEIFKSLDMMARNVLIHLKSVKSMOPDYLPPDVSDGFEQVRELR 113
59 VQVTHSPPOKLEIFKSLDMMARNVLIHLKSVKSMOPDYLPPDVSDGFEQVRELR 118
Db 59 VQVTHSPPOKLEIFKSLDMMARNVLIHLKSVKSMOPDYLPPDVSDGFEQVRELR 118

QY 114 RAKEIPDDYFVVLVGDMTTEALPTYQTMNLTDGVRDEFGASPTSMALWTRAMTAENR 173
119 RAKEIPDDYFVVLVGDMTTEALPTYQTMNLTDGVRDEFGASPTSMALWTRAMTAENR 178
Db 119 RAKEIPDDYFVVLVGDMTTEALPTYQTMNLTDGVRDEFGASPTSMALWTRAMTAENR 178

QY 174 HGDLLNKYLLSGRVDMRKIEKTIQYLLSGMDIKSENSPYLGFTYSFOERATFISHAN 233
179 HGDLLNKYLLSGRVDMRKIEKTIQYLLSGMDIKSENSPYLGFTYSFOERATFISHAN 238
Db 179 HGDLLNKYLLSGRVDMRKIEKTIQYLLSGMDIKSENSPYLGFTYSFOERATFISHAN 238

QY 234 TAKLAQHYGDKNLAHICGSIASDEKRRHATYTKIVEKLAIEDPTTVIAFADMMRRKTTM 293
239 TARQKHEGDIKLAQICGTIADKREHETAYTKIVEKLEIDPDGTVLAFADMMRRKTTM 298
Db 239 TARQKHEGDIKLAQICGTIADKREHETAYTKIVEKLEIDPDGTVLAFADMMRRKTTM 298

QY 294 PAHLMYDGSDELLFKHFTAVAQRYVXSALDYCDILEFLVQKNNVERLTGLSDEGRKAOE 353
299 PAHLMYDGRDNLDFHFSAAQRLGVYAKDYADILEFLVGRKVKDLTGLSDEGRKAOE 358
Db 299 PAHLMYDGRDNLDFHFSAAQRLGVYAKDYADILEFLVGRKVKDLTGLSDEGRKAOE 358

QY 354 YVCELGPRIKRVVEEKVQGEKKKAEHP--VSFSWTFNRELKI 394
359 YVCLRPRIKRVVEERAKRAK----EAPTFMFSMTFDROVKL 396
Db 359 YVCLRPRIKRVVEERAKRAK----EAPTFMFSMTFDROVKL 396

RESULT 4
US-08-329-560-3
; Sequence 3, Application US/08329560
; Patent No. 5654402
; GENERAL INFORMATION:
; APPLICANT: CAHOON, Edgar B.
; APPLICANT: OHLROGE, John B.
; TITLE OF INVENTION: Methods and Compositions Relating to
; TITLE OF INVENTION: Plant 6-Delta Palmitoyl-Acyl Carrier Protein Desaturase
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pioneer Hi-Bred International, Inc.
; STREET: 700 Capital Square, 400 Locust Street
; CITY: Des Moines
; STATE: Iowa
; COUNTRY: US
; ZIP: 50309
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/329,560
; FILING DATE: 26-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Yates, Michael E.
; REGISTRATION NUMBER: 36,063
; REFERENCE/DOCKET NUMBER: 0284US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (515) 248-4800
; TELEFAX: (515) 248-4844
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 396 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-329-560-3

Query Match 72.3%; Score 1490; DB 1; Length 396;
Best Local Similarity 71.1%; Pred. No. 8e-143;
Matches 286; Conservative 50; Mismatches 52; Indels 14; Gaps 5;

QY 1 MALKN-FCKKNNPAAFAKSPLEPVTVSSPRVPMASSTVNSMVLNDLKSP-----PN 53
1 MALKNFLSQTKLPSPALPMASTR--SPKFTMASTLKSCKSEVENLKKPFMPPREVH 58
Db 1 MALKNFLSQTKLPSPALPMASTR--SPKFTMASTLKSCKSEVENLKKPFMPPREVH 58

QY 54 LQVTHSPPOKLEIFKSLDMMARNVLIHLKSVKSMOPDYLPPDVSDGFEQVRELR 113
59 VQVTHSPPOKLEIFKSLDMMARNVLIHLKSVKSMOPDYLPPDVSDGFEQVRELR 118
Db 59 VQVTHSPPOKLEIFKSLDMMARNVLIHLKSVKSMOPDYLPPDVSDGFEQVRELR 118

QY 114 RAKEIPDDYFVVLVGDMTTEALPTYQTMNLTDGVRDEFGASPTSMALWTRAMTAENR 173
119 RAKEIPDDYFVVLVGDMTTEALPTYQTMNLTDGVRDEFGASPTSMALWTRAMTAENR 178
Db 119 RAKEIPDDYFVVLVGDMTTEALPTYQTMNLTDGVRDEFGASPTSMALWTRAMTAENR 178

QY 174 HGDLLNKYLLSGRVDMRKIEKTIQYLLSGMDIKSENSPYLGFTYSFOERATFISHAN 233
179 HGDLLNKYLLSGRVDMRKIEKTIQYLLSGMDIKSENSPYLGFTYSFOERATFISHAN 238
Db 179 HGDLLNKYLLSGRVDMRKIEKTIQYLLSGMDIKSENSPYLGFTYSFOERATFISHAN 238

QY 234 TAKLAQHYGDKNLAHICGSIASDEKRRHATYTKIVEKLAIEDPTTVIAFADMMRRKTTM 293
239 TARQKHEGDIKLAQICGTIADKREHETAYTKIVEKLEIDPDGTVLAFADMMRRKTTM 298
Db 239 TARQKHEGDIKLAQICGTIADKREHETAYTKIVEKLEIDPDGTVLAFADMMRRKTTM 298

QY 294 PAHLMYDGSDELLFKHFTAVAQRYVXSALDYCDILEFLVQKNNVERLTGLSDEGRKAOE 353
299 PAHLMYDGRDNLDFHFSAAQRLGVYAKDYADILEFLVGRKVKDLTGLSDEGRKAOE 358
Db 299 PAHLMYDGRDNLDFHFSAAQRLGVYAKDYADILEFLVGRKVKDLTGLSDEGRKAOE 358

QY 354 YVCELGPRIKRVVEEKVQGEKKKAEHP--VSFSWTFNRELKI 394
359 YVCLRPRIKRVVEERAKRAK----EAPTFMFSMTFDROVKL 396
Db 359 YVCLRPRIKRVVEERAKRAK----EAPTFMFSMTFDROVKL 396

RESULT 5
US-08-471-791-16
; Sequence 16, Application US/08471791
; Patent No. 5723595
; GENERAL INFORMATION:
; APPLICANT: Thompson, Gregory A
; APPLICANT: Knaut, Vic C
; TITLE OF INVENTION: Plant Desaturases-Compositions
; TITLE OF INVENTION: and Uses
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calgene, Inc.
; STREET: 1920 Fifth Street
; CITY: Davis
; STATE: California
; COUNTRY: USA
; ZIP: 95616
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.1
; SOFTWARE: Microsoftword 5.1 (a)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,791
; FILING DATE: 6-JUNE-95
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/762,762
; FILING DATE: 16-SEPT-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/01746
; FILING DATE: 14-MAR-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/615,784
; FILING DATE: 14-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/567,373
; FILING DATE: 13-AUG-1990


```

: STREET: 1920 Fifth Street
: CITY: Davis
: STATE: California
: COUNTRY: USA
: ZIP: 95616
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB storage
: COMPUTER: Apple Macintosh
: OPERATING SYSTEM: Macintosh 6.0.7
: SOFTWARE: Microsoft Word 4.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US91/01746
: FILING DATE: 19910314
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/615,784
: FILING DATE: 14-NOV-1990
: APPLICATION NUMBER: 07/567,373
: FILING DATE: 13-AUG-1990
: APPLICATION NUMBER: 07/494,106
: FILING DATE: 16-MAR-1990
: ATTORNEY/AGENT INFORMATION:
: NAME: Lassen, Elizabeth
: REGISTRATION NUMBER: 31,845
: NAME: Donna E. Scherer
: REGISTRATION NUMBER: 34,719
: REFERENCE/DOCKET NUMBER: CGNE 69-3.WO
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (916) 753-6313
: TELEFAX: (916) 753-1510
: TELEX: 350370 CGNE
: INFORMATION FOR SEQ ID NO: 16:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 396 amino acids
: TYPE: AMINO ACID
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: PCT-US91-01746-16

Query Match          72.3%; Score 1490; DB 5; Length 396;
Best Local Similarity 71.1%; Pred. No. 8e-143;
Matches 286; Conservative 50; Mismatches 52; Indels 14; Gaps 5;

QY 1 MALKIN-FOCKKRNHPAAKSPLPVTRVSSPRFMASTVNSNVLNLSKSP-----PN 53
DB 1 MALKINPFLSQOKLPSPALPPEMASTR--SPKFYMASTLKSKEVENLKKPEMPREVA 58
QY 54 LQVTHSMFPQKLEIFKSLDDMARNNVLIHLKSEKSMQPODYLPDPVSGFEQVELRE 113
DB 59 VQVTHSMFPQKLEIFKSLDDMARNNVLIHLKSEKSMQPODYLPDPVSGFEQVELRE 118
QY 114 RAKELPDDYFVVLVGDMTTEALPTYMSMLNRCDGIDETGAEPSSAMWTRMTAEENR 173
DB 119 RAKELPDDYFVVLVGDMTTEALPTYMSMLNRCDGIDETGAEPSSAMWTRMTAEENR 178
QY 174 HGDLNLKLYLSGRVDMRKIEKTIQYILGSGMDIKSENSPYLGFIYTSFOERATFTSHAN 233
DB 179 HGDLNLKLYLSGRVDMRKIEKTIQYILGSGMDIKSENSPYLGFIYTSFOERATFTSHAN 238
QY 234 TAKLAQNHGDKRLAHICGSIASDEKRNHATATYTKIYEKLEIDPDTTVIAFADMRKKITM 293
DB 239 TARQAKREHGDKRLAHICGSIASDEKRNHATATYTKIYEKLEIDPDTTVIAFADMRKKITM 298
QY 294 PAHLMYDSDELLEFKHFTAVAOQVYXSALDYCDLLEFLVDMWNERLGLSDEGRKAOE 353
DB 299 PAHLMYDSDELLEFKHFTAVAOQVYXSALDYCDLLEFLVDMWNERLGLSDEGRKAOE 358
QY 354 YVCELGPKIRAEKVEKQEKRRKKAHP--VSESWIFNRELKI 394
DB 359 YVCELGPKIRAEKVEKQEKRRKKAHP--VSESWIFNRELKI 396

RESULT 8
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US-07-995-657-6
: Sequence 6, Application US/07995657
: Patent No. 5443974
: GENERAL INFORMATION:
: APPLICANT: Hiltz, William D.
: APPLICANT: Yadav, Narendra S.
: APPLICANT: Perez, Luis
: TITLE OF INVENTION: Nucleotide Sequence of
: TITLE OF INVENTION: Soybean Stearoyl-ACP
: NUMBER OF SEQUENCES: 7
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: E. I. du Pont de Nemours
: ADDRESSEE: and Company
: STREET: 1007 Market Street
: CITY: Wilmington
: STATE: Delaware
: COUNTRY: U.S.A.
: ZIP: 19898
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
: COMPUTER: Macintosh
: OPERATING SYSTEM: Macintosh System, 6.0
: SOFTWARE: Microsoft Word, 4.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/995,657
: FILING DATE: 19921211
: FILING DATE: C) CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: GEIGER, KATHLEEN W.
: REGISTRATION NUMBER: 35,880
: REFERENCE/DOCKET NUMBER: BB_1022-B
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 302-892-8112
: TELEFAX: 302-892-7949
: TELEX: 835420
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 391 amino acids
: TYPE: AMINO ACID
: STRANDEDNESS: unknown
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-07-995-657-6

Query Match          69.7%; Score 1436.5; DB 1; Length 391;
Best Local Similarity 68.5%; Pred. No. 2.1e-137;
Matches 278; Conservative 44; Mismatches 53; Indels 31; Gaps 4;

QY 1 MALKINPQCKKRNHPAAKSPLPVTRVS-----SPRFMASTVNSNVLNLSKSP- 51
DB 1 MALKINPQCKKRNHPAAKSPLPVTRVS-----SPRFMASTVNSNVLNLSKSP- 51
QY 52 -----PRLQVTHSMFPQKLEIFKSLDDMARNNVLIHLKSEKSMQPODYLPDPVSGFE 106
DB 47 TPRREVHVQVTHSMFPQKLEIFKSLDDMARNNVLIHLKSEKSMQPODYLPDPVSGFE 106
QY 107 QVRELRAKEIPDDYFVVLVGDMTTEALPTYMSMLNRCDGIDETGAEPSSAMWTR 166
DB 107 QVRELRAKEIPDDYFVVLVGDMTTEALPTYMSMLNRCDGIDETGAEPSSAMWTR 166
QY 167 WTAENRHGDLNLKLYLSGRVDMRKIEKTIQYILGSGMDIKSENSPYLGFIYTSFOERA 226
DB 167 WTAENRHGDLNLKLYLSGRVDMRKIEKTIQYILGSGMDIKSENSPYLGFIYTSFOERA 226
QY 227 TFSHGNTAKLAKENHGDKRLAHICGSIASDEKRNHATATYTKIYEKLEIDPDTTVIAFAD 286
DB 227 TFSHGNTAKLAKENHGDKRLAHICGSIASDEKRNHATATYTKIYEKLEIDPDTTVIAFAD 286
QY 287 MRRKITMPAHLMYDGSDELLEFKHFTAVAOQVYXSALDYCDLLEFLVDMWNERLGLSLD 346
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INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 396 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-471-791-13

Query Match
Best Local Similarity 67.1%; Pred. No. 2,7e-134;
Matches 271; Conservative 54; Mismatches 61; Indels 18; Gaps 5;

QY 1 MALKL---NFQCKKHHPAFAKSPLPVTRVSSPRVFMASTVNSNMYLDNLKSP----- 51
D 1 MALRTPVTLQSERYSFSPKK---ANLRSPKFMASTLGSSTPKVDNAKRFQPPRE 56
QY 52 PNLQVTHSMPPQKLEIFKSLDDMARNNVLIHLKSVESKQPODYLPDPVSDGFEQVREL 111
D 57 VHVQVTHSMPPQKLEIFKSLDDMARNNVLIHLKSVESKQPODYLPDPVSDGFEQVREL 116
QY 112 REAKEIPDDYFVVLVGMITEEALPTYMSMLNRCGDKETGAEPSAMAMTWTAAE 171
D 117 RARAKEIPDDYFVVLVGMITEEALPTYMSMLNRCGDKETGAEPSAMAMTWTAAE 176
QY 172 NRHGLLKKLYLSGRVDMRKIEKTIQYILIGSGMDIKSENSPYLGFTYSFOERATFISH 231
D 177 NRHGLLKKLYLSGRVDMRKIEKTIQYILIGSGMDIKSENSPYLGFTYSFOERATFISH 236
QY 232 ANTKLAOHGDKNLAHICGSIASDEKRRHATYATKIVEKLAIEDPTTVIAFADMRRKI 291
D 237 GNTARHAADHGDVKAQICGTIASDEKRRHATYATKIVEKLAIEDPTTVIAFADMRRKI 296
QY 292 TMPAHLMTYDGSDELLFKHFTVAQORVXYVSALDYCDILEFLVDKMNVERLTGSDGSKRA 351
D 297 SMPAHLMTYDGRDNLFEHFSVAQORVXYVSALDYCDILEFLVDKMNVERLTGSDGSKRA 356
QY 352 QEVYVCELGPRIKIRVEKVGKERRKKAHP-VSFSWTFNRELKI 394
D 357 QDVYVCELGPRIKIRVEKVGKERRKKAHP-VSFSWTFNRELKI 396

RESULT 11
US-08-926-522-2
Sequence 2, Application US/08926522
Patent No. 6426447
GENERAL INFORMATION:
APPLICANT: Vic C. Knauf
APPLICANT: Gregory A. Thompson
TITLE OF INVENTION: PLANT SEED OILS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
CITY: Davis
STATE: CA
COUNTRY: USA
ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: Microsoft Word 5.1(a)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/926,522
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/458,173
FILING DATE: 2-June-1995
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth Lassen
REGISTRATION NUMBER: 31,845
NAME: Donna E. Scherer

REGISTRATION NUMBER: 34,719
NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: CGNE DES
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 396 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-926-522-2

Query Match
Best Local Similarity 67.1%; Pred. No. 2,7e-134;
Matches 271; Conservative 54; Mismatches 61; Indels 18; Gaps 5;

QY 1 MALKL---NFQCKKHHPAFAKSPLPVTRVSSPRVFMASTVNSNMYLDNLKSP----- 51
D 1 MALRTPVTLQSERYSFSPKK---ANLRSPKFMASTLGSSTPKVDNAKRFQPPRE 56
QY 52 PNLQVTHSMPPQKLEIFKSLDDMARNNVLIHLKSVESKQPODYLPDPVSDGFEQVREL 111
D 57 VHVQVTHSMPPQKLEIFKSLDDMARNNVLIHLKSVESKQPODYLPDPVSDGFEQVREL 116
QY 112 REAKEIPDDYFVVLVGMITEEALPTYMSMLNRCGDKETGAEPSAMAMTWTAAE 171
D 117 RARAKEIPDDYFVVLVGMITEEALPTYMSMLNRCGDKETGAEPSAMAMTWTAAE 176
QY 172 NRHGLLKKLYLSGRVDMRKIEKTIQYILIGSGMDIKSENSPYLGFTYSFOERATFISH 231
D 177 NRHGLLKKLYLSGRVDMRKIEKTIQYILIGSGMDIKSENSPYLGFTYSFOERATFISH 236
QY 232 ANTKLAOHGDKNLAHICGSIASDEKRRHATYATKIVEKLAIEDPTTVIAFADMRRKI 291
D 237 GNTARHAADHGDVKAQICGTIASDEKRRHATYATKIVEKLAIEDPTTVIAFADMRRKI 296
QY 292 TMPAHLMTYDGSDELLFKHFTVAQORVXYVSALDYCDILEFLVDKMNVERLTGSDGSKRA 351
D 297 SMPAHLMTYDGRDNLFEHFSVAQORVXYVSALDYCDILEFLVDKMNVERLTGSDGSKRA 356
QY 352 QEVYVCELGPRIKIRVEKVGKERRKKAHP-VSFSWTFNRELKI 394
D 357 QDVYVCELGPRIKIRVEKVGKERRKKAHP-VSFSWTFNRELKI 396

RESULT 12
PCT-US91-01746-13
Sequence 13, Application PC/TUS9101746
GENERAL INFORMATION:
APPLICANT: Thompson, Gregory A
APPLICANT: Knauf, Vic C
TITLE OF INVENTION: Plant Desaturases-Compositions and Uses
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
CITY: Davis
STATE: California
COUNTRY: USA
ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.7
SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/01746
FILING DATE: 19910314
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/615,784
FILING DATE: 14-NOV-1990
APPLICATION NUMBER: 07/567,373
FILING DATE: 13-AUG-1990
APPLICATION NUMBER: 07/494,106
FILING DATE: 16-MAR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Lassen, Elizabeth
REGISTRATION NUMBER: 31,845
NAME: Donna E. Scherert
REGISTRATION NUMBER: 34,719
REFERENCE/DOCKET NUMBER: CGNE 69-3 WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
TELEX: 350370 CGNE
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 396 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US91-01746-13

Query Match 68.2%; Score 1406; DB 5; Length 396;
Best Local Similarity 67.1%; Pred. No. 2.7e-134;
Matches 271; Conservative 54; Mismatches 61; Indels 18; Gaps 5;

QY 1 MALKL---NFQCKNHFAAFKSPPLVTRVSSPRVFMASTVNSMVLNLSKSP-----P 51
DB 1 MALRITPTVLOSERKRSFEPKK---ANLRSKRFMASTIGSTSKVDNAKRPFPQPRE 56
QY 52 PMLQVTHSMPPQKLEIFKSLDDMARNVLIHLKSVESWQPDYLPDVSDFGEQVREL 111
DB 57 VHVQVTHSMPPQKLEIFKSLDDMARNVLIHLKSVESWQPDYLPDVSDFGEQVREL 116
QY 112 RRRAKEIPDQVYVVLVDGMTTEALPTVMSLNRCDIGDENGAESAVAMTRATTAEE 171
DB 117 RRAKEIPDQVYVVLVDGMTTEALPTVMSLNRCDIGDENGAESAVAMTRATTAEE 176
QY 172 NRHGLDLNKLYLISGRVDMRKIEKTIQYLLISGMDIKSENSPYLGFTYSFOERATFISH 231
DB 177 NRHGLDLNKLYLISGRVDMRKIEKTIQYLLISGMDIKSENSPYLGFTYSFOERATFISH 236
QY 232 ANFALAQHYGCKNLIAHIGSISASDEKRRHATYTKIVEKLAELIDPDTVIAEADMMRKTI 291
DB 237 GNTAHADHGDGVKLAQICGTIASDEKRHETAYTKIVEKLEIDPDGTVLAFAADMMRKTI 296
QY 292 TMPAHIMYDGSDELLEFKHFTVAORVXYVSALDYCDILEFVDMKMWVERLTGSDGGRKA 351
DB 297 SMPAHIMYDGSDELLEFKHFTVAORVXYVSALDYCDILEFVDMKMWVERLTGSDGGRKA 356
QY 352 QEYVCELGPKIRVEKVOGKEKKKAEPH-VFSFWIENRELI 394
DB 357 QDYVCGLPPIRIRLEBAGRAK----EGPVVPFWSWIFRQYKL 396

RESULT 13
US-08-471-791-20
Sequence 20, Application US/08471791
Patent No. 5723595
GENERAL INFORMATION:
APPLICANT: Thompson, Gregory A
APPLICANT: Knaut, Vic C
TITLE OF INVENTION: Plant Desaturases-Compositions
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
CITY: Davis
STATE: California
COUNTRY: USA

ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: Microsoft Word 5.1 (a)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,791
FILING DATE: 6-JUNE-95
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/762,762
FILING DATE: 16-SEPT-1991
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/615,784
FILING DATE: 14-NOV-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/567,373
FILING DATE: 13-AUG-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/494,106
FILING DATE: 16-MAR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Lassen, Elizabeth
REGISTRATION NUMBER: 31,845
NAME: Donna E. Scherert
REGISTRATION NUMBER: 34,719
NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: CGNE 69-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
TELEX: 350370 CGNE
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 398 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-471-791-20

Query Match 67.7%; Score 1396; DB 1; Length 398;
Best Local Similarity 66.9%; Pred. No. 2.8e-133;
Matches 269; Conservative 55; Mismatches 66; Indels 12; Gaps 4;

QY 1 MALKLNFQCKK--NHPAAFKSPPLVTRVSSPRVFMASTVNSMVLNLSKSP-----P 52
DB 1 MALKLNPASQPRNPFSS-ARPISTFRSPKFLCLASSSSALSSKEVESLAKKPTTPKEV 59
QY 53 NLQVTHSMPPQKLEIFKSLDDMARNVLIHLKSVESWQPDYLPDVSDFGEQVREL 112
DB 60 HVGVLHSMPPQKLEIFKSLDDMARNVLIHLKSVESWQPDYLPDVSDFGEQVREL 119
QY 113 ERKKEIPDQVYVVLVDGMTTEALPTVMSLNRCDIGDENGAESAVAMTRATTAEE 172
DB 120 ERKKEIPDQVYVVLVDGMTTEALPTVMSLNRCDIGDENGAESAVAMTRATTAEE 179
QY 173 RHHDDLNLNKLYLISGRVDMRKIEKTIQYLLISGMDIKSENSPYLGFTYSFOERATFISH 232
DB 180 RHHDDLNLNKLYLISGRVDMRKIEKTIQYLLISGMDIKSENSPYLGFTYSFOERATFISH 239
QY 233 NTAKLAQHYGCKNLIAHIGSISASDEKRRHATYTKIVEKLAELIDPDTVIAEADMMRKTI 292
DB 240 NTAKLAQHYGCKNLIAHIGSISASDEKRRHATYTKIVEKLAELIDPDTVIAEADMMRKTI 299
QY 293 MPAHIMYDGSDELLEFKHFTVAORVXYVSALDYCDILEFVDMKMWVERLTGSDGGRKA 352


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Db      60  HVQVLSMPPQKIEIFKSMEDNAEQNLLTQLKOVEKSWQPODFLPDPASDGFEDQVRELR 119
Qy      113  ERAKEIPDDYFVVLVGDMTTEALPTYSMLNRCDG IKDETGAEPSSANAMWTRAWTAEN 172
Db      120  ERARELPDDYFVVLVGDMTTEALPTYOQMTMLNTLDGVDETGASPTSWAITWRAWTAEN 179
Qy      173  RHGDLINKYLYLSGRVDMRKIEKTIQYLLIGSGMDIKSENSPYLGFITYTSFOERATFISHA 232
Db      180  RHGDLINKYLYLSGRVDMRKIEKTIQYLLIGSGMDPRTENNPPYLGFIYTSFOERATFISHG 239
Qy      233  NTAQIAQHYGDKNLAHIGSIADEKRHATAVTYKIVEKLAIEDPDTTVAIAFADMRRKIT 292
Db      240  NTAQIAQHYGDKNLAHIGSIADEKRHATAVTYKIVEKLAIEDPDTTVAIAFADMRRKIT 299
Qy      293  MPAHLMYDGSDELLFKHFTAVAOQVXYVSALDYCDILLEFLVDRKWNVERLTGLSDEGRKAQ 352
Db      300  MPAHLMYDGRDESLFNFSSVAQRLGVYTAQDYADILLEFLVGRWKIESLTGLSGEGNKAQ 359
Qy      353  EYVCELGPKIRVREEKYQGEKKKKAHHPVSFSMIFNRELKI 394
Db      360  EYLCGLTPRIRLDERAQARAKGP--KVPFSWIHDREVOL 398

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Search completed: December 1, 2002, 21:22:08
 Job time : 20 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 1, 2002, 21:12:16 ; Search time 2407 Seconds
(without alignments)
9043.097 Million cell updates/sec

Title: US-09-732-597-1
Perfect score: 1344
Sequence: 1 caaccacagaataaataa.....tttgagtttaagtaaaaaa 1344

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estbda:*
2: em_estbhum:*
3: em_estlin:*
4: em_estlmu:*
5: em_estloy:*
6: em_estlpl:*
7: em_estlro:*
8: em_estlrc:*
9: gb_estl1:*
10: gb_estl2:*
11: gb_estl3:*
12: gb_estl4:*
13: gb_estl5:*
14: gb_estl6:*
15: em_estfun:*
16: em_estlom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_man:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	513	38.2	1780	11	AY104235
2	491.2	36.5	1623	11	AY104301
3	424.4	31.6	702	13	BM436665
4	382.6	28.5	708	13	BI271942
5	372.2	27.7	712	12	BG269539
6	368.8	27.4	699	14	B0027980

7	368.6	27.4	804	10	BE559272	BE559272	HV_CEB002
8	360	26.8	641	10	AV933496	AV933496	
9	358.8	26.7	811	10	BE643410	BE643410	Cr12_8_L12
10	355	26.4	628	10	AW509087	AW509087	s139h08.y
11	353.4	26.3	852	14	B0510820	B0510820	EST618235
12	351	26.1	1055	12	BG837910	BG837910	Zml0_10c0
13	343.2	25.5	671	10	AV914373	AV914373	
14	341.8	25.4	612	9	AT730379	AT730379	BMLG1676
15	341.6	25.4	606	10	BE610498	BE610498	sq77b04.y
16	340.8	25.4	634	14	B0149496	B0149496	NE105B07F
17	340.6	25.3	619	13	BM323364	BM323364	PICT_18.D
18	339.8	25.3	593	13	BI425553	BI425553	sa132910.
19	338.8	25.2	793	12	BG888941	BG888941	EST514792
20	332.8	24.8	596	10	AV934363	AV934363	AV934363
21	331	24.6	633	13	BI179928	BI179928	EST520873
22	321.4	23.9	793	12	BG887868	BG887868	EST513719
23	321.2	23.9	636	10	AW395273	AW395273	sh46a10.y
24	321.2	23.9	662	9	AJ432511	AJ432511	
25	319.4	23.8	621	13	BJ464232	BJ464232	
26	318.4	23.7	655	10	AW066113	AW066113	687006D02
27	317.6	23.6	569	13	BM322551	BM322551	PICT_6_C0
28	314.2	23.4	566	13	BI468759	BI468759	sa103a07.
29	313.8	23.3	971	12	BG446852	BG446852	GA_Eb003
30	310	23.1	556	13	BI674398	BI674398	sa171907.
31	309.8	23.1	752	13	BI933357	BI933357	EST533246
32	305.2	22.7	763	13	BI934897	BI934897	EST554786
33	304.6	22.7	650	10	BE427627	BE427627	PSR7275.I
34	302.8	22.5	885	12	BF268770	BF268770	GA_Eb000
35	302.4	22.5	604	13	BJ481070	BJ481070	
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37	301.8	22.5	714	12	BG889927	BG889927	EST515778
38	300.4	22.4	622	10	BE517215	BE517215	WHE0615_C
39	299.4	22.3	708	14	BQ802244	BQ802244	WHE2823_G
40	296.4	22.1	736	13	BJ247775	BJ247775	
41	295.2	22.0	700	12	BG596559	BG596559	EST495237
42	294.2	21.9	561	10	AW030327	AW030327	EST723582
43	294	21.9	745	14	BQ112398	BQ112398	EST597974
44	291.2	21.7	576	12	BG352880	BG352880	sa192e03.
45	291	21.7	745	13	BJ167132	BJ167132	

ALIGNMENTS

RESULT 1	AY104235	1780 bp	mRNA	linear	HTC 25-MAY-2002
LOCUS	AY104235				
DEFINITION	Zea mays PCO105183 mRNA sequence.				
ACCESSION	AY104235				
VERSION	AY104235.1	GI:21207313			
KEYWORDS	HTC.				
SOURCE	Zea mays.				
ORGANISM	Zea mays.				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC Clade; Panicoideae; Andropogoneae; Zea.				
AUTHORS	1 (bases 1 to 1780) Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S., Arthur,L.W., Hanatey,M., Morgante,M. and Tingey,S.V.				
TITLE	Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes				
JOURNAL	Unpublished (2002)				
AUTHORS	2 (bases 1 to 1780) Coe,E.C.				
TITLE	Direct Submission				
JOURNAL	Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA				
FEATURES	Location/Qualifiers				
source	1..1780 /organism="Zea mays" /db_xref="MaizeDB:636088" /db_xref="taxon:4577" /clone="PCO105183"				

Db 498 TGAGAGACCTTACCTACATACCAACATGCTTACACTCTTGATGGAGTCCGGATCA 557
Qy 501 GACTGGGGCTGAGCCAGCTGCTTGGGCAATGTGACTAGGCGATGAGTCCGGAAGAGA 560
Db 558 AACTGCTGCAAGTCCACACGAGCGGCTTGGACAAAGGCGATGAGACGTGGAAGAGA 617
Qy 561 TAGACATGCTGCTTCCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 620
Db 618 CAGACATGCTGCTTCCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 677
Qy 621 AATTGAGAGACTATTCATATCTCATGCGCTCAGAGATGATCAAGTCAAGTCAAGTCA 680
Db 678 AATTGAGAGACTATTCATATCTCATGCGCTCAGAGATGATCAAGTCAAGTCAAGTCA 737
Qy 681 CCCCTACCTAGGCTTCAATCTACATCTCTTCCAGAGAGAGACCTTCAATATCCATCC 740
Db 738 CCCCTACCTAGGCTTCAATCTACATCTCTTCCAGAGAGAGACCTTCAATATCCATCC 797
Qy 741 CACACACACCAAGCTGGCCCAACACTAGCGGACAAAGAACCTGCTCAGATCTGGGCTC 800
Db 798 GAATTAAGTCAAGGCAAGGCAAGGAGATGATGATCTCAAGCTGGGCGCAGATATGTGGC 857
Qy 801 CATGCGCTCCGAGAGAGCGCCAGCCACAGCTACACAGATGCTGGAAGAGCTGCG 860
Db 858 GATGACAGCCGATGAGAGAGCGCCAGCCAGCCAGCTACACAGATGCTGGAAGAGCTT 917
Qy 861 TGAGATGACCCCGACACACAGATTAATGCTTTTGCATATGATGCGCAAAATAATAC 920
Db 918 CGAGATGACCCCGATTAACAGAGTGTGCTTGTGCTGATGATGAGAGAGATGATC 977
Qy 921 AATGCGACGCACTTGTATGATGATGATGATGATGATGATGATGATGATGATGATG 980
Db 978 GATGCGACCCGATTCATGATGATGATGATGATGATGATGATGATGATGATGATG 1037
Qy 981 GATGCGACCCGATTCATGATGATGATGATGATGATGATGATGATGATGATGATG 1040
Db 1038 GATGCGACCCGATTCATGATGATGATGATGATGATGATGATGATGATGATGATG 1097
Qy 1041 GGTGATTAATGGAATGTGGAAGAGCTTACGAGGCTGTGCGAGAGGCGGAAAGCGCA 1100
Db 1098 GGTGATTAATGGAATGTGGAAGAGCTTACGAGGCTGTGCGAGAGGCGGAAAGCGCA 1157
Qy 1101 GGAATATGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1160
Db 1158 GGAATATGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1217
Qy 1161 GAG 1220
Db 1218 GAG 1268
Qy 1221 GAGATATGAG 1253
Db 1269 GAGATATGAG 1301

RESULT 3
BMA36665 702 bp mRNA linear EST 31-JAN-2002
LOCUS VVA008A04.52913 An expressed sequence tag database for abiotic
DEFINITION stressed leaves of Vitis vinifera var. Chardonnay Vitis vinifera
ACCESSION BMA36665
VERSION BMA36665.1 GI:18458387
KEYWORDS EST.
SOURCE Vitis vinifera.
ORGANISM Vitis vinifera.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Vitaceae; Vitis.
1 (bases 1 to 702)
Cramer, G.R. and Cushman, J.C.
An expressed sequence tag database for abiotic stressed leaves of
Vitis vinifera var. Chardonnay

JOURNAL Unpublished (2002)
COMMENT Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR Primers
FORWARD: T3 20mer
BACKWARD: T7 21mer
Plate: 008 row: A column: 04
Seq primer: T3 20mer
High quality sequence stop: 702.
Location/Qualifiers
1..702
/organism="Vitis vinifera"
/db_xref="taxon:29760"
/clone_lib="VVA008A04"
/clone_lib="An expressed sequence tag database for abiotic
stressed leaves of Vitis vinifera var. Chardonnay"
/issue_type="leaf"
/dev_stage="juvenile and adult"
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1:
EcoRI; Site_2: XhoI; Library construction was performed
according to Stratagene's recommended protocol for the
Lambda UniZapXR vector and cDNA synthesis kit."
BASE COUNT 210 a 144 c 176 g 172 t
ORIGIN
Query Match 31.6%; Score 424.4; DB 13; Length 702;
Best Local Similarity 75.5%; Pred. No. 9.1e-79;
Matches 527; Conservative 0; Mismatches 171; Indels 0; Gaps 0;
Qy 259 GATGATGGGCTGGAACATGATGATGATGATGATGATGATGATGATGATGATGATG 318
Db 2 GAAATATGGGCTGGAACATGATGATGATGATGATGATGATGATGATGATGATGATG 61
Qy 319 CCACAGAGACTTGTGCGGATCCGGTGTGACAGAGATTCGAGAGAGCAAGTGGCGAGTTG 378
Db 62 CCACAGAGATTTTACAGATTCCTGCTGTGATGATGATGATGATGATGATGATGATGAT 121
Qy 379 AGGGAAGGCGCAAGAGATTCGCCAGCAGTATTTGTGTGATGATGATGATGATGATG 428
Db 122 AGGGAAGGCGCAAGAGATTCGCCAGCAGTATTTGTGTGATGATGATGATGATGATG 181
Qy 439 ACAG 498
Db 182 ACTGAG 241
Qy 499 GAGACTGGGCTGAGCCAGTGTGCGCAATGTGAGTGGGATGAGTGGGATGAGTGGGATG 558
Db 242 GAAACAGGTGCAAGGCTCAGCTTCTGAGCAATTTGGACAGAGGCGATGAGTGGGATG 301
Qy 559 AATGACAGTGTGAGCTTCTCAATTAAGTACCTTTATTTGTCTGGAAGGTTGATAGG 618
Db 302 AACAGCATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 361
Qy 619 AAATTTGAGAGAGAGTTCATATATCTCATGCGCTCAGAGATGATGATGATGATGATG 678
Db 362 CAATTTGAGAGAGAGTTCATATATTTGATGATGATGATGATGATGATGATGATGATG 421
Qy 679 AGGCGCTACCTAGGCTTCAATCTACATCTCTTCCAGAGAGAGAGAGAGAGAGAGAGAG 738
Db 422 AGTCCTACTCGGGTTCAATCTACATCTCTTCCAGAGAGAGAGAGAGAGAGAGAGAG 481
Qy 739 GCCACACAGCAAGTGGCCCAACACTGACGAGCAAGCAAGTGGCTGCTCATCTGCGGC 798
Db 482 GGCACACTGCGCAGGATGCCCAAGAGCATGGGATATGAAGTTGGCTCAATATATG 541
Qy 799 TCCATGCTTCGACAGAGAGAGGCGCACAGCTTACACCAAGATCTGCGAAAGCTC 838
Db 542 ACAATTTGCTCAAGATGAGAGAGGCGCATGAAGCTGACCAAGATATGCAAAAGCTC 601

QY	859	GCTGGATGACCCCGACACAGCAATGCTTTTCGATGATGCGCAAAATA	918
Db	602	TTTTGATTTGATTCCTGATGGAAGTGTGCTTCTGCTGACATGATGAGGAAATTC	661
QY	919	ACAATCCAGCCACTTGATGTACGACGGAAGTGACGA	956
Db	662	TCTATGCTGCTACCTGATGTATGATGCGCGTGATGA	699
RESULT 4			
LOCUS	Bi271942		
DEFINITION	Bi271942	708 bp	linear
ACCESSION	Bi271942	EST	EST 18-JUL-2001
VERSION	Bi271942.1		
KEYWORDS	EST.		
ORGANISM	barrel medic.		
	Medicago truncatula		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eustosids I; Fabales; Fabaceae; Papilionoideae; Trifoliales; Medicago.		
REFERENCE	1 (bases 1 to 708)		
AUTHORS	Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Imman, J.T., Wellner, J.W. and May, G.D.		
TITLE	Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula flower library		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: May GD Plant Biology Division The Samuel Roberts Noble Foundation 2510 Sam Noble Parkway, Ardmore, OK 73402, USA Tel: 580 221 7391 Fax: 580 221 7380 Email: gdmay@noble.org Insert Length: 708 Std Error: 0.00 Plate: 016 row: F column: 09 Seq primer: TCACACAGGAACACGCTATGAC. Location/Qualifiers		
FEATURES			
SOURCE	1. 708 /organism="Medicago truncatula" /db_xref="taxon:3880" /clone="NF016F09FL" /clone_lib="Developing flower" /tissue_type="Developing flowers" /dev_stage="Developmentally pooled. Contains a mixture of very young, developing, fully-opened flowers and flowers in early transition into pods." /note="Vector: Lambda zap; cDNA was prepared from polyA+ RNA from very young, developing, fully-opened flowers and flowers transitioning into pods. The cDNA was directionally ligated into the Uni-zap XR vector (Stratagene) and packaged using the GigaPack III Gold packaging extracts. Phagemids containing cDNA inserts were in vivo excised from the recombinant Uni-zap XR vector using ExAssist helper phage and the E. coli strain XL1-Blue MRF' (Stratagene). Excised plasmids were plated using SOLR cells."		
BASE COUNT	194 a	137 c	181 g
ORIGIN		190 t	6 others
Query Match	28.5%;	Score 382.6;	DB 13;
Best Local Similarity	71.0%;	Pred. No. 5.1e-70;	Length 708;
Matches 502;	Conservative 0;	Mismatches 205;	Indels 0;
		Gaps 0;	
QY	406	GACATTTTGGGGTGTGTTGAGATATGATGACAGAAAGCACTTCACATATATG	465
Db	1	GATTACTTTGTTGTTCTGCTGATGATATGGTCACAGAAAGCTCTTCTACTTACCA	60
QY	466	TCTATGCTCAATAGCTGTGATGATTAAGATGAGACTGGGGCTGAGCCCACTGCTGG	525

Db	Accession	Source	Organism	Reference Title	Journal Comment
Db	61	ACTATGCTTAATACCTTTGGACGAGGTCTGTATGAAACAGGTCGACGCCCTACTCCCTAG			
QY	526	GCAATGTGACTTAGGGCATAGCACTGCGCCGAAAGATAGACATGTGTAACCTTCTCAATAG			
Db	121	GCTATTGTGACCAAGACATGACAGCTGGAAGAAATAGACAGGTATCTTTAAACAAG			
QY	586	TACCTTTATTTTGTCTCGAAGGGTGTGATATGAGAAATATGAGAAAGCTATTCATAATTCAC			
Db	181	TATCTTTACTTCTCCGGGGCGGTGTGATATGACACAAATTTGAAAGCAATTCAGTACTTG			
QY	646	ATCGGCTCAGGAATGGATATCAAGTCAGAAACAGCCCTACCTAGCTTCACTACACA			
Db	241	ATTGGCTCTGGAATGGATCTCGGACTGAGAAATAGCCCTTACCTGGCTTATATCTACACT			
QY	706	TCCTTCCAAGAAAGAACCTTTCATATCCCATGCGCACACAGCCAGCTGGCCCAACAC			
Db	301	TCATTTCAAGAGAGGGCAACCTTTATATGCAATGGAAACACAGCTAAGGCTTCTAAGAA			
QY	766	TACGGCGCAACAAAGCTGCTGCATCATCTGCGGCTCCATCGCGACAGCAAGCCAC			
Db	361	CGCGGCGATTTGAAGTGGCTGAGATCTGTGTCGTGATTCCTCGATATAGAAACGCCAT			
QY	826	GCCACAGCTTACACCAAGATGCTGGAAGAGCTGCTGAGATGACCCGACACACAGTA			
Db	421	GAGACTGCTTACACAAAGATAGTGGAAAAAGCATTTGAAATGATCTGATGGAACAGTT			
QY	886	ATTGCTTTTGGCATATGATGTCGCAAAAAAATACAAATCCAGCGCACTTGATATACGAC			
Db	481	ATTGCTTTTGGCATATGATGTCGCAAAAAAATACAAATCCAGCGCACTTGATATACGAC			
QY	946	GGAACTGACGAACCTCTTTTAAACATTTCCACGGGGTGTCTCAGAGATGNGGGTTTAT			
Db	541	GCGCCAGACGAACAATCTGTTGATTAATCAATCTGCTGTCGCCAGGCAATGGAAGCTAC			
QY	1006	TCTGCGTTGGATATATTGGACACATCTTAAGAGTTTCTGTGTGTGATTAATGATATGGAAAG			
Db	601	ACTGCGCAAGGACTATGCTGATATATCTGTTGTTGTGTGCGGAGGAGGGAAGGCGAC			
QY	1066	CTTACGGGGGCTGTCGACGAGGGGCGAAAGCGCAGATATGTGTG			
Db	661	ATAACCGGACTTTCAGGTGANGACNAAGGCACAGAGATATGTTG			
RESULT 5					
LOCUS	BG269539	712 bp	mRNA	linear	EST 20-FEB-2001
DEFINITION	L0-3624T3 Ice plant Lambda Uni-Zap XR expression library, 0 hours				
KEYWORDS	NaCl treatment Mesembryanthemum crystallinum cDNA clone L0-3624 5',				
ACCESSION	BG269539				
VERSION	BG269539.1	GI:12975736			
SOURCE	EST.				
ORGANISM	common iceplant.				
	Mesembryanthemum crystallinum				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;				
	Caryophyllales; Caryophyllales; Aizoaceae; Mesembryanthemum.				
REFERENCE	Cushman, J.C.				
AUTHORS	1 (bases 1 to 712)				
TITLE	An expressed sequence tag database for the common ice plant,				
	Mesembryanthemum crystallinum				
JOURNAL	Unpublished (1997)				
COMMENT	Contact: Cushman JC				
	Department of Biochemistry				
	University of Nevada				
	MS2001, Reno, NV 89557-0014, USA				
	Tel: 775-784-1918				
	Fax: 775-784-1650				
	Email: jcushman@unr.edu				
	PCR Primers				
	FORWARD: T7				
	BACKWARD: T3				

QY 513 GCCCAGTCTTGGSCAATGTGGAGTACGGGCTGCGGACGAGATAGATAGTGTGA 572
 Db 246 CCGTACTTCTTGGCTATCTGCTGCGCTTGGACCGCTGAGAAAAACAGCAGCGTGA 305
 QY 573 CTTTCTCAATAGTACCTTTATTTGTCTGGAAGGGTGTGATGAGGAAATTTGAGAAC 632
 Db 306 TCTTTTCATCATGATTTGATTTAGTACGGGGGCTGACATGAGGACGATTCAGAAAC 365
 QY 633 TATTCATATTCATGCTGCTCAGCAATGATATCAAGTCAAGAAACAGCCCTACTAGG 692
 Db 366 AATTACGTACCTCATTTGCTGCTGATGAGAACCCCGGACCGAAGAAACAGTCTTACCTGG 425
 QY 693 CTTTCACTTACATCTCTTCCAGAGAGACGACCTTATATCCATGCCACAGCCAA 752
 Db 426 GTTCACTTACATCTTCAATTTAGAGCGCTGCCACCTCATCTCTACGAAACACAGCCCG 485
 QY 753 GCTGGCCCAACACTACGAGGACCAAGAACCTGCTGACATCTGCGGCTCCATCGCTCCGA 812
 Db 486 GCACGCAAGAGAGACATGTTACGTAAGCTGCTCAATGTGCGGATTAATTTGAGCTGA 545
 QY 813 CGAAGAGCGCCAGCCACAGCCTACACCAAGATCTGTGAAAGCTGCTGAGATGACCC 872
 Db 546 TGAAGAAGAGGACGAAACCCCTACACAAATAGTGAAGAACTCTTCGAAATTTGACCC 605
 QY 873 CGACACACAGTAACTCTTTTGCAGATATGATGCGCAAAAATAACAAATGCCAGCGCA 932
 Db 606 GAGAGGCGACTTCTGCTTTTGTCTGACATGATNGAGAAAGATCTCTCATGCTGCACA 665
 QY 933 CTTGATGTACGACGAGAGTACGACACTTCTTT 965
 Db 666 CTTGATGTACGAGTGGCGTACCATTAACCTTT 698

RESULT 7
 BE559272 804 bp mRNA linear EST 23-OCT-2001
 LOCUS BE559272
 DEFINITION HV_CEB0023F16f Hordeum vulgare seedling green leaf EST library
 HV_CEB0023F16f, mRNA sequence.
 ACCESSION BE559272
 VERSION BE559272.2 GI:13266511
 KEYWORDS EST.
 SOURCE Hordeum vulgare.
 ORGANISM Hordeum vulgare.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
 ; Triticeae; Hordeum.
 1 (bases 1 to 804)
 Wing, R., Close, T.J., Kleinbols, A., Wise, R., Wei, F., Begum, D.,
 Fritsch, D., Yu, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi
 , D.W., Fenton, R.D., Oates, R. and Main, D.
 Development of a genetically and physically anchored EST resource
 for barley genomics: Blumeria infected incompatible (Mla6) seedling
 leaf cDNA library
 Unpublished (2001)
 On Aug 14, 2000 this sequence version replaced gi:9823678.
 JOURNAL COMMENT
 CONTACT: Wing RA
 Clemson University Genomics Institute
 100 Jordan Hall, Clemson, SC 29634, USA
 Tel: 864 656 7288
 Fax: 864 656 4293
 Email: twing@clemson.edu
 Total bp bases = 569
 Seq primer: AATTAACTCTCACTTAAGGG
 High quality sequence stop: 696.

FEATURES
 source
 1..804
 location/Qualifiers

/organism="Hordeum vulgare"
 /cultivar="C116151 (Mla6)"
 /db_xref="taxon:4513"
 /clone="HV_CEB0023F16f"
 /clone_lib="Hordeum vulgare seedling green leaf EST

library HVCDNA0005 (Blumeria challenged)"
 /issue_type="seedling green leaf"
 /lab_host="SOLR"
 /note="Vector: LambdaZAP; Site_1: EcoRI; Site_2: XhoI;
 C.I. 16151 (Mla6) plants were greenhouse grown in the R
 Wise lab at Iowa State University, Ames, IA; 7 day old
 green seedlings were challenged with isolate 5874 (AvrMla6
) of Blumeria graminis f. sp. hordei, and leaves were
 harvested 20 and 24 hr post-inoculation and snap frozen;
 uninoculated leaves were harvested 20 hr post-inoculation
 (Wei, Wise). In the TJ Close lab at the University of
 California, Riverside, total RNA was prepared from each
 sample pool, equal quantities of all three RNA pools were
 combined, poly(A) RNA was purified from the mixture, one
 primary unamplified cDNA library was made, and 1 million
 pfu were in vivo excised to give pBluescript SK(-) cDNA
 phagemids (Choi, Close). Phagemids were plated and picked
 at the Clemson University Genomics Institute (CUGI) (Begum
 , Palmer, Fritsch, Atkins and Wing). Plasmid DNA
 preparations, DNA sequencing and sequence analysis were
 performed at CUGI (Wing, Yu, Fritsch, Henry, Simmons, Oates
 , Rambo, Main). The sequence has been trimmed to remove
 vector sequence and contains a minimum of 100 bases of
 phred value 20 or above. For more details on library
 preparation and sequence analysis see
 http://www.genome.clemson.edu/projects/barley. To order
 this clone see http://www.genome.clemson.edu/orders. Also
 see Close TJ, Wing R, Kleinbols A, Wise R (2001)
 Genetically and physically anchored EST resources for
 barley genomics. Barley Genetics Newsletter 31:29-30.
 (http://wheat.pw.usda.gov/gppages/bgn/31/cover.html)"
 BASE COUNT 239 a 194 c 184 g 187 t
 ORIGIN

Query Match 27.4%; Score 368.6; DB 10; Length 804;
 Best Local Similarity 68.8%; Pred. No. 4.4e-67;
 Matches 506; Conservativity 0; Mismatches 229; Indels 0; Gaps 0;
 QY 203 ATCTCAAGTCACTCATCTATGTCACCCCAAAAGCTAGAAATTTCAAGTCCCTTATG 262
 Db 70 ATCTCCAGATCATGATCTACTACCTACGACACAAAGCAGAGATCTTGTATTCATTAAT 129
 QY 263 ATTGGGCTAGAACCAATGTGTGATTCACCTCAATCTGTCGAAATCTTGGACACAC 322
 Db 130 CTTGGGCTAGGAGCAACCTTTGTAAGCTTGTGAAGCAGTTGAGAACTCATGCGAGCAC 189
 QY 323 AAGACTTCTTCCGGATCCGGTGTACAGCGATTCGAGAGCAAGTCCGGAGTTGAGGG 382
 Db 190 AGGACTTCTTCCAGAGACCCCTTCTCCGAGGAGTTTATGTAAGTAAAGAACTGAGGG 249
 QY 383 AAGGGGCAAGGAGATTTCCCGAGGACATATTTGTGGTGTAGTTGGAGATATGATCAG 442
 Db 250 AGCGGGCAAGGAAATCTCGATGACACTTGTGGTGTAGTTGGTGTGATGATGATCTG 309
 QY 443 AAGAGCACTTCCACATATATGTCTATATGCTCAATAGTGTGATTAAGATAGAGA 502
 Db 310 AGGAAGCCCTTCTACTACCAACAATGCTCAACACCTTGTATGTTGCTCCGAGATGAA 369
 QY 503 CTGGGGCTAGAGCCAGTCTGGGCAATGTGACATAGGCGATGAGTCCGAAAGAGATA 562
 Db 370 CTGGCGCAAGCCCACTGCTGGGCTGTTGGCAAGAGATGAGTCTGAGAAAGAAACA 429
 QY 563 GACATGTGACCTTTCATTAATGTAATCTTATTTGTCTGGAAGGGTGTATAGAGAAA 622
 Db 430 GCGATGTGATCTTCTGAAACAGTATATGATCTTTCAGACGCGGTGATGATGACAAA 489
 QY 623 TTGAGAAGACTATTCATATCTCATGCGCTCAGAGATGATCAAGTCAAGAAAGAGCC 682
 Db 490 TTGAGAAGACTATTCATATCTCATGCGCTCAGAGATGATCAAGTCAAGAAAGAGCC 549
 QY 683 CTTACTAGGCTTCACTTACATCTCTTCCAGAGAGAGACCTTCAATATCCATGCGCA 742
 Db 550 CTTACTAGGCTTCTTCTTACATCTTCCAGAGAGAGACCTTCAATATCCATGCGCA 609

Query Match 26.7%; Score 358.8; DB 10; Length 811;
 Best Local Similarity 65.4%; Pred. 4.9e-65;
 Matches 522; Conservative 0; Mismatches 276; Indels 0; Gaps 0;

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OY 352 GGAATTCGAGAGCAAGTCCGGAGTTGAGGCAAGGCGCAAGGAGATTCGCCGACGACTAT 411
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2 GGAATTCCTGAGATGAGTTAAAGACAGACACCGTCCGAGCAATTCACCGATGATAC 61
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 412 TTGTGCTGTTAGTTGAGATGATGATCAGAGAAAGACATCTCCACATATATGCTATG 471
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 62 CTGTGCTGCTGCTAGGGGATATGATATACGAAAGACCCCTTCGACTTATACAGACCATG 121
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 472 CTCATAGTGTGTATGATTAAGATGAGAGTGGGGCTGAGCCCACTGCTTGGCGAATG 531
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 122 CTGAAACACTCTGGATGGAGTTCGTGATGTGACTGAGCAAGCCACATCGTGGCGCAGG 181
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 532 TGGACATAGGCGCATGAGTCCGCAAGAGAAATAGACATGTGACCTTCATTAAGTACTT 591
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 182 TGGACTGAGAGCTTGACTGCTGAAGAAATAGGCAATGATCTCTGAAACAAATATCTT 241
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 592 TATTTGCTGGAAGGTTGATGAGAAATAGAGAACTATTCATATTCATGCGGC 651
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 242 TATCTTACTGGAAGAGTGGATGATGAGAGTATGAGAGAACTATACAGTACCTGATTTG 301
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 652 TCAGGAATGGAATVCAAGTCAAGAAACAGCCCTACCTAGGCTTCATCTACATCCCTC 711
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 302 TCTGGAATGGATCCACAACAGAAATAGCCCTTATTTGGTTTCATCTACTTCTCTT 361
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 712 CAAGAGAGGCAACCTTCATATCCCATGCCAACAAGCCAGCTGGCCCAACACTACGGC 771
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 362 CAAGAGAGGCAACCTTCTGTTCTCAAGGTAATACGCCAGGCAAGAAAGATTGCT 421
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 772 GACAAAGACTCGCTCATCATCTCGGCTCCATCGCCTCCAGCAGAAAGCCGACGCCACA 831
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 422 GACTTAAAGCTTCACAGATCTCTGGATATATTCAGCTGATGAAGACCTCATGAAAT 481
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 832 GCTTACACCAAGATGCTGGAAGAGCTGCTGAGATGAGACCCGACACACAGTAATTC 891
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 482 GCATATACAGAGATGTTGGAAGAGCTCTTTGAACTTGATTCAGTGAATGACTATCT 541
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 892 TTTGCGATATGATGCGCAAAAAAATAACATCCAGCGCACTTGATGACGCGAAGT 951
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 542 TTAGAGAGATGATGAGAAAGAAATATCCATGCCACACCTGATGATGATGCGCAAT 601
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 952 GACGAACTCTTTTAAACATTTACGCGGCTGCTCAGAGAGTGGGCTTATTCGCG 1011
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 602 CATAGAACATCTTTCAACAATTTCTCTGTTGCAAAAGACAGAGAGTACACTGCT 661
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 1012 TTGATTTATTCGACATCTTAGAGTTCTGTTGGATTAATGAATGTGAAAGGCTTACG 1071
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 662 AAGGACTATGACAGATATTTTGGAGCATCTGTCAAACGATGGAATGAGAAACTATCT 721
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 1072 GGGCTTCGAGACAGGCGCAAAAGCGCAGAGATATGTGTCAATTTGGTCCCAAGATT 1131
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 722 GGACATTCAGAGAGGCGCAACACCAAGCTCAAGACTATGTGTAACTAGCTAATCTGATA 781
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 1132 AGCGAGTGAAGAGAAA 1149
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 782 AGGAAGCTAGAGAGAGA 799
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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RESULT 10
 AWS09087 628 bp mRNA linear EST 03-DEC-2001
 LOCUS s13908.y1 Gm-r1030 glycine max cDNA clone GENOME SYSTEMS CLONE ID:
 DEFINITION Gm-r1030-1336 5' similar to SW:STAD_SOYBN 042807 ACYL-L-ACYL-CARRIER
 PROTEIN] DESATURASE PRECURSOR ; mRNA sequence.
 ACCESSION AWS09087
 VERSION AWS09087.1 GI:7147165
 KEYWORDS EST.
 SOURCE soybean.
 ORGANISM Glycine max

REFERENCE
 AUTHORS Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Coryell,V., Khanna
 A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
 Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
 Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schuck
 R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., Mccann
 R., Waterson,R. and Wilson,R.
 Public Soybean EST Project
 Unpublished (1999)
 CONTACT: Shoemaker R/Public Soybean EST Project
 Public Soybean EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available through: ResGen, Invitrogen Corp. 2130
 South Memorial Parkway Huntville, AL 35801 For further information
 call: (800)-533-4363 or contact via email: ccu@resgen.com
 Insert Length: 1443 Std Error: 0.00
 High quality sequence stop: 441.
 Location/Qualifiers
 1..628
 /organism="Glycine max"
 /db_xref="taxon:3847"
 /clone="GENOME SYSTEMS CLONE ID: Gm-r1030-1336"
 /clone_1ib="Gm-r1030"
 /lab_host="DH10B"
 /note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; This
 cDNA library was constructed from mRNA isolated from
 immature cotyledons of greenhouse grown plants
 (individual seed fresh weight of 100-300mg). The library
 was prepared using the Life Technologies pSuperScript cDNA
 library construction kit. Complementary DNA was
 synthesized from mRNA using a poly(dT) sequence with a
 NotI restriction site. SalI linkers adapters were ligated
 to the blunt-ended cDNA fragments followed by NotI
 digestion. The cDNA fragments were directionally cloned
 into the NotI-SalI restriction site of the pSPORT1
 vector. The ligated cDNA fragments were transformed into
 E. coli Electromax DH10B host cells. This library was
 constructed by Dr. Lila Vodkin and Dr. Ann Khanna. Note
 that Gm-r1030 is a re-track of Gm-cl007."

BASE COUNT 187 a 126 c 163 g 152 t
 ORIGIN

Query Match 26.4%; Score 355; DB 10; Length 628;
 Best Local Similarity 72.9%; Pred. No. 3.1e-64;
 Matches 457; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

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OY 321 ACAAGACTACTCCGATCCGATCGGTGCAGAGATTCGAGAGCAAGTGGGAGTTGAG 380
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Db 1 ACAGAGATTTTATACCGACCCCTCCAGATGATTTGAAGACCAAGTGAAGAACTGAG 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 381 GGAAGAGGCCAAGAGATTCGCCAGACACTATTTTGTGTGTTAGTTGAGATATGATCAC 440
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 AGAGAGAGCAAAAGAGATTCAGATGATGATTTGTTGTTCTTGCGAGACATGATCATC 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 441 AGAAGAAAGCACTTCCAAATATATGCTATGCTCAATAGTGTGATGCTTAAAGATGA 500
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 AGAGGAAGCTCTCTTACCGACCTTACCAACTATGTTAAATACTTGGATGAGACTTGTGATGA 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 501 GACTGGGCTGAGCCAGCTGCTGCGCAATGTGAGTGAAGGCAATGAGCTCCCAAGAGAA 560
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 AACAGGTCCAGCGCTTACTCTCTGGGCAATTTGGACAAGGCGATGAGCTGCTTAAGAAAA 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 561 TAGACATGTGACCTTCTCAATTAAGTACTTATTTGTCTGGAAGGTTGATATGAGGAA 620
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 CAGACACGGTGATCTTCTTAACAAATATATCTGTACTTGAGTGGAGAGTTGACATGAACA 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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QY 621 AATTGAGAGACTATTCAATATCTCATCGGCTCAGGATGATATCAAGTCAGAAAACAG 680
|||||
Db 301 AATTGAGAGAAATTCAGTACCTTATTTGGTGTGGATGATCTCGGACCGAGAAACAG 360
QY 681 CCCCTACCTAGGCTTCATCTACATCTCTTCCAGAGAGAACACTTATATCCCATG 740
|||||
Db 361 CCCCTACCTAGGCTTCATCTACATCTCTTCCAGAGAGAACACTTATATCCCATG 420
QY 741 CAACACAGCAAGCTGGCCCAACACTACGGGCAACAAGACCTCGTACATCTGCGGCTC 800
|||||
Db 421 AAACACAGGCGAGGCTTGGCAAGAGAGATGATGACATATAATTTGGCAGATCTGCGGCTC 480
QY 801 CATCGCTTCGAGAGAAAGCGCCAGCCACAGCTACACCAAGATGCTGAAAAGCTCGC 860
|||||
Db 481 GATTCGCTAGATGAGAAAGCGCCAGAGACTGATACACAAAGATGATGAAAAGCTGTG 540
QY 861 TGAGATCGACCCCGACACACAGTATTCCTTTTGGAGATATGATGCGCAAAAAATTAAC 920
|||||
Db 541 TGAGGCTGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 600
QY 921 AATGCGAGCGACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 947
|||||
Db 601 TATGCCAGCACACTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 627

RESULT 11
B0510820 852 bp mRNA linear EST 22-JUL-2002
LOCUS
DEFINITION EST618235 Generation of a set of potato CDNA clones for microarray
analyses mixed potato tissues Solanum tuberosum CDNA clone STMHN19
5' end, mRNA sequence.
B0510820
ACCESSION
VERSION B0510820.2 GI:21926503
KEYWORDS
SOURCE EST
ORGANISM
Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asterales; easterids I; Solanales; Solanaceae; Solanum.
1 (bases 1 to 852)
REFERENCE
AUTHORS Buell,C.R., Hart,A., Baker,B., Tanksley,S., Fry,W., Smart,C.,
Karamycheva,S.A., Griffiths,H., van der Hoeven,R., Tsai,J. and
Karamycheva,S.A.
TITLE Generation of a set of potato CDNA clones for microarray analyses
JOURNAL Unpublished (2002)
COMMENT On Jun 10, 2002 this sequence version replaced gi:21369689.
Other ESTs: EST618236
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potatodt@igrr.org
This clone is available through the Research Genetics, contact the
Research Genetics for further information 1-800-711-6195 or
cdna@resgen.com
Seq primer: T3.
Location/Qualifiers
1..852
/organism="Solanum tuberosum"
/cultivar="Kennebec or Binjle"
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microarray analyses mixed potato tissues"
/tissue.type="mixed tissues"
/lab.host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; supplier: Combination of untreated and Phytophthora
infestans-treated libraries of stolons, leaves, leaflets,
axillary buds of stem explants, petioles, germinating eyes
tubers, or roots."

BASE COUNT 236 a 184 c 208 g 224 t
ORIGIN

Query Match 26.3%; Score 353.4; DB 14; Length 852;
Best Local Similarity 73.1%; Pred. No. 6,6e-54;
Matches 467; Conservative 0; Mismatches 171; Indels 1; Gaps 1;
QY 203 ATCTTCAAGTCACTCACTATGTCACACCCCAAAAGCTAGAAATTTCAATCCCTTATG 262
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Db 212 ATTTTAAATTTTCTTCACTTCCATCCCGCAAGAACCTTTGATTTGATCCCTGATG 271
QY 263 ATTTGGCTAGAACAAATGTTTGTATTCCTCAATATGTCGAAATTTTGGCAACAC 322
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Db 272 GTTTGGCTAGAACAAATGTTTGTATTCCTCAATATGTCGAAATTTTGGCAACAC 331
QY 323 AGACTACTTTCGCGGATCCGCTGTCAGACGATTCGAGAGCAAGTCGCGGATTTAGG 382
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Db 332 GTGACTTTTCTTCGATCCGTCAGAACGATTTGAAAGCAAGTCGAGAGATTTGGCAGGCA 391
QY 383 AAGGGCGAAGAGATTTCCGAGACATTTTGTGTGTTAGTTGAGATATGATCACAG 442
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Db 392 AGAGGTGCAAGAAATTCGATGATGATGATGATGATGATGATGATGATGATGATGATG 451
QY 443 AAGAGCACTTCCACATATATGTCATGTCATATAGTGTGATGATGATGATGATGATG 502
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Db 452 AGAGGCTTTCACACTTATGACACATGCTTACACCTGATGATGATGATGATGATGATG 511
QY 503 CTGGGCTGAGCCAGTGTGGCAATGTGCACTAGGCACTGAGCTGCCGAGAGATA 562
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QY 563 GACATGTGACCTTTCATATAGTACCTTTATTTGTGAGAGGTTGATATGAGAAA 622
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QY 623 TTGAGAGACTATTTCAATATGTCATGCTCAGAGATGATGATGATGATGATGATGATG 682
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Db 631 TTGAGAGACTATTTCAATATGTCATGCTCAGAGATGATGATGATGATGATGATGATG 690
QY 683 CTTACCTAGGCTTCATCTACATCTCTTCCAGAGAGAGAACCTTCATATCCCATG 742
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Db 691 CGTATGCTGTTTATGCTACACTTCTTCCAGAGAGAGGCTACCTTCATTTTCATGAA 750
QY 743 ACACAGCAAGCTGCGCCCAACACTACGCGCAGACAACTTCCTCATCTGCGGCTCA 802
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Db 751 ATACAGCTCGCATGCTACAGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 810
QY 803 TTGCTGCGAGAGAGAGCGCCAGCGCCACAGCTACACCA 841
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RESULT 12
BG837910 1055 bp mRNA linear EST 25-MAY-2001
LOCUS
DEFINITION Zm10_10c08_A Zm10_AARC_ECORC_Fusarium_graminearum_corn_silk Zea
mays CDNA clone Zm10_10c08, mRNA sequence.
BG837910
ACCESSION
VERSION BG837910.1 GI:14204233
KEYWORDS
SOURCE EST
ORGANISM
Zea mays.
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 1055)
REFERENCE
AUTHORS Harris,L.J., Balcerzak,M., Allard,S., Saparno,A., Couroux,P., De
Moors,A., Hattori,J.T., Ouellet,T., Robert,L.S., Singh,J.A., Sprolt
D. and Tinker,N.A.
TITLE Expressed Sequence Tags from Maize Silk Six Hours After Silk
Channel Inoculation with Fusarium graminearum
JOURNAL Unpublished (2001)
COMMENT Contact: Harris, Linda J.
Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-Food Canada

Bl09. 21, Central Experimental Farm, Ottawa, Ontario, KIA 0C6,
CANADA
Tel: (613) 759-1314
Fax: (613) 759-6566
Email: harristj@em.agr.ca.

FEATURES

source

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/cultivar="CO388"
/db_xref="taxon:4577"
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BASE COUNT 279 a 231 c 295 g 246 t 4 others
ORIGIN

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Best Local Similarity 68.7%; Pred. No. 2.1e-63;
Matches 496; Conservative 3; Mismatches 214; Indels 9; Gaps 1;

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DB 28 TTGACAGGGCATRACACTGAGAGAACATGCTGACCTCTTACAGTACATG 87

OY 592 TATTTGCTGAGAGGCTTATATGAGAAATTGAGAAGACTATTCATATCTCATCGGC 651

DB 88 TTGCTTACTGAGCGGCTGACATGAAACAATTGAGAAGCMTACATATCTGATTGGT 147

OY 652 TCAGGATGATATCAAGTCAGAAACGCCCTTACTAGGCTTCATCTACATCTTC 711

DB 148 TCCGGATGATCTCGAATGAGAACACCCCTTCTGGTTTCTCTACACATATTC 207

OY 712 CAAGAGAGCAACCTTCATATCCATGCGCAACACAGCCAGCGCCCAACTACGCG 771

DB 208 CAAGAAGGGCAACATTTGTGCGATGGAATACGCAAGCATGCCAAGAGATAGT 267

OY 772 GACAAAGACCTGCTCACAATGCGGCTCCATCGCTCCGACGAGAAGCGCCACG 831

DB 268 GATCTCAACCTGCGCAGATATGTGGCAGATAGCAGCGATGAGAAGCGCCACG 327

OY 832 GCCTACACCAAGTGTGAAAAAGTCGCTGATGACGCCGCCACACAACTATTCGT 891

DB 328 GCCTACACCAAGTGTGAAAAAGTCGCTGATGACGCCGCCACACAACTATTCGT 387

OY 892 TTTGAGATATGATGCGCAAAAAAATACATATGCCAGCCACTTGATGACGAGAGT 951

DB 388 TTTGCGATATGATGAGAAAGATCAGATGCCAGCCCATCTATGATACGAGGTAAG 447

OY 952 GACGAACCTCTTTTAAACATTTACAGCGGTTGCTCAGAGAGTGGGTTTATTCGCG 1011

DB 448 GACGAACCTCTCTGAGCACTTACAGCGGTTGCTCAGAGAGTGGGTTTATTCGCG 507

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DB 508 AAAGACTATGCGGACATCTCGAGTTCTGATCCAGAGGCGAAATCGCGGAGCTACA 567

OY 1072 GGGCTGTGCGAGAGGCGGAAAGCGCAGAAATATGTTGTAATTGGTCCAGATT 1131

DB 568 GGGCTGTGCGAGAGGCGGAAAGCGCAGAAATATGTTGTAATTGGTCCAGATT 627

OY 1132 AGCGAGTGAAGAGAAATGCAAGGGAAGAGAGAGAAAGAAAGCTGAGCAACCTGTT 1191

DB 628 AGCGGCTGATATGAGCTCAAGCAGGCGCAAGCA-----AGCACCGGTTATT 678

OY 1192 TCTTTCAGCTGATTTTCATATCGGAGGTGATGATGACAGAGGAGGAGATGGA 1251

DB 679 CCTTCAGTTGGGTTTATGACCGCAAGGTGACGCTTATATCAGAACGCTTAGCAATGTG 738

OY 1252 GG 1253

DB 739 GG 740

RESULT 13

AV914373 671 bp mRNA linear EST 18-JAN-2002

LOCUS AV914373 K. Sato unpublished cDNA library, cv. Haruna NiJo

DEFINITION germination shoots Hordeum vulgare subsp. vulgare cDNA clone

bag55007 5', mRNA sequence.

ACCESSION AV914373.1 GI:18210150

VERSION AV914373

KEYWORDS EST.

SOURCE Hordeum vulgare subsp. vulgare.

ORGANISM Hordeum vulgare subsp. vulgare.

REFERENCE Sato, K., Saitoh, D. and Takeda, K.

AUTHORS Barley EST sequencing project in NIG and Okayama Univ

TITLE Unpublished (2002)

JOURNAL Contact: Tadasi Shin-1

COMMENT Center For Genetic Resource Information

National Institute of Genetics

111 Yata, Mishima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6856

Fax: 81-559-81-6855

Email: tshin@genes.nig.ac.jp.

LOCATION/Qualifiers

1..671

/organism="Hordeum vulgare subsp. vulgare"

/cultivar="Haruna NiJo"

/db_xref="taxon:112509"

/clone="bag55007"

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Query Match 25.5%; Score 343.2; DB 10; Length 671;

Best Local Similarity 69.5%; Pred. No. 9.2e-62;

Matches 465; Conservative 0; Mismatches 204; Indels 0; Gaps 0;

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DB 3 GAGAAGNTTGGCAGCCAGCACTTCTTCAAGACCCCTTCTCGAGGAGATTATGATGA 62

OY 366 AGTGGGAGTTTGAAGGAAGGCGCAAGAGATTTCCGAGACATATTTGTGGTTAGT 425

DB 63 AGTAAAGAACTGAGGAGGAGGCAAGAAATCCCTGATGACTACTTGTGGCTAGT 122

OY 426 TGGAGATATGATGCAAGAAAGACACTTCCACATATATGTCTATGCTCAATAGTGTGA 485

DB 123 TGGTACATGTGTTACGTAGAGAACCCCTTCTTACTACTACCAACATGCTCAACACCTTGA 182

OY 486 TGGTATTAAGATGAGACTGGGCTGAGCCACTGCTTGGGCAATGTGACTAGGCGATG 545

DB 183 TGGTGTCCGAGATGAACATGGCCCAAGCCCAACTGCTGGGCTGTTGCTGACAGAGCATG 242

OY 546 GACTGCCGAAGAGAAATGACATGTGATCTTCAATATATACCTTATTTGTTGGAAG 605

DB 243 GACTGCTGAAGAAACAGCAGTGTGATCTTGAACAAAGTATATGATACCTTTCAGAGAGC 302

South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
High quality sequence stop: 417.

FEATURES
source

QY	888	TGCT	891
Db	603	GGCT	606

Search completed: December 2, 2002, 00:40:21
Job time : 2417 secs

BASE COUNT	181 a	128 c	143 g	154 t
ORIGIN				

Query Match	25.48;	Score 341.6;	DB 10;	Length 606;
Best Local Similarity	72.88;	Pred. No. 2e-61;		
Matches 440;	Conservative 0;	Mismatches 164;	Indels 0;	Gaps 0;

[illegible]

GenCore version 5.1.3
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OH nucleic - nucleic search, using sw model

Run on: December 1, 2002, 21:12:16 ; Search time 76 Seconds

(without alignments)
5423.336 Million cell updates/sec

Title: US-09-732-597-1

Perfect score: 1344

Sequence: 1 caaccacagaataataaat.....tttgagtttaagtaaaaaa 1344

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents.NA.*

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6: /cgn2_6/ptodata/2/lna/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	613.4	45.6	1309	US-07-926-788A-1	Sequence 1, Appl
2	572	42.6	1668	US-08-471-791-15	Sequence 15, Appl
3	572	42.6	1668	US-08-926-522-3	Sequence 3, Appl
4	572	42.6	1668	US-08-926-522-3	Sequence 15, Appl
5	522	38.8	1533	US-07-721-761A-32	Sequence 32, Appl
6	522	38.8	1533	US-07-978-687-32	Sequence 32, Appl
7	522	38.8	1533	US-08-471-791-12	Sequence 12, Appl
8	522	38.8	1533	US-08-926-522-1	Sequence 1, Appl
9	522	38.8	1533	US-08-926-522-1	Sequence 12, Appl
10	522	38.8	1533	US-08-926-522-1	Sequence 12, Appl
11	521.2	38.8	2243	US-07-995-657-1	Sequence 1, Appl
12	521.2	38.8	2243	US-08-474-587-1	Sequence 1, Appl
13	513	38.2	1621	US-08-679-645-1	Sequence 1, Appl
14	511.8	38.1	1495	US-08-471-791-19	Sequence 19, Appl
15	511.8	38.1	1495	US-08-926-522-5	Sequence 5, Appl
16	511.8	38.1	1495	US-08-926-522-5	Sequence 19, Appl
17	426.4	31.7	1272	US-08-869-137-1	Sequence 1, Appl
18	393.8	29.3	1258	US-08-539-798-1	Sequence 1, Appl
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20	112	8.3	176	US-07-721-761A-34	Sequence 34, Appl
21	112	8.3	176	US-07-978-687-34	Sequence 34, Appl
22	112	8.3	176	US-08-471-791-18	Sequence 18, Appl
23	112	8.3	176	US-08-471-791-18	Sequence 18, Appl
24	112	8.3	176	US-08-471-791-18	Sequence 18, Appl
25	64.8	4.8	7218	US-08-232-463-14	Sequence 14, Appl
26	57.6	4.3	143	US-08-471-791-43	Sequence 43, Appl
27	57.6	4.3	143	US-08-926-522-7	Sequence 7, Appl

28	57.6	4.3	143	5	PCR-US91-01746-43	Sequence 43, Appl
29	40.6	3.0	225	1	US-08-471-791-14	Sequence 14, Appl
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31	40.4	3.0	1926	4	US-09-249-585A-2	Sequence 2, Appl
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33	40.4	3.0	2580	4	US-09-359-081-2	Sequence 2, Appl
34	40.4	3.0	5452	2	US-09-130-114-1	Sequence 1, Appl
35	40.4	3.0	9600	4	US-08-910-647-1	Sequence 1, Appl
36	40.4	3.0	9600	4	US-09-620-925-1	Sequence 1, Appl
37	40.4	3.0	10596	1	US-07-884-811-15	Sequence 15, Appl
38	40.4	3.0	10596	1	US-07-885-971-15	Sequence 15, Appl
39	40.4	3.0	10596	1	US-08-087-783A-15	Sequence 15, Appl
40	40.4	3.0	10596	1	US-08-194-088B-15	Sequence 15, Appl
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43	39	2.9	1856	2	US-08-360-606B-29	Sequence 29, Appl
44	38	2.8	289	4	US-09-007-005-17	Sequence 17, Appl
45	38	2.8	289	4	US-09-244-796-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-07-926-788A-1
Sequence 1, Application US/07926788A
Patent No. 5430134
GENERAL INFORMATION:
APPLICANT: John B. Ohlroge, Edgar B.
APPLICANT: Cahoon, John Shanklin,
TITLE OF INVENTION: A Method For
TITLE OF INVENTION: Production of Petroselinic Acid and 12
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ian C. McLeod
STREET: 2190 Commons Parkway
CITY: Okemos
STATE: Michigan
COUNTRY: USA
ZIP: 48864
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 5.25 inch, 360 kb
MEDIUM TYPE: storage
COMPUTER: Acer
OPERATING SYSTEM: MS-DOS (version 3.3)
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/926, 788A
FILING DATE: 19920807
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Ian C. McLeod
REGISTRATION NUMBER: 20,931
REFERENCE/DOCKET NUMBER: MSU 4.1-156
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 347-4100
TELEFAX: (517) 347-4103
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1309 Base Pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: Double
TOPOLOGY: Linear
MOLECULE TYPE:
DESCRIPTION: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:

ORGANISM: Coriandrum sativum
IMMEDIATE SOURCE:
LIBRARY: CDNA
US-07-926-788A-1

Query Match 45.6%; Score 613.4; DB 1; Length 1309;
Best Local Similarity 77.0%; Pred. No. 6.6e-166;
Matches 762; Conservative 0; Mismatches 222; Indels 6; Gaps 1;

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OY 301 GTCGAAATCTTGGCAGCAACAAGACTACTTCCGATCCGATCCGATCAGACGATTCGAG 360
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OY 601 GGAAGGTTGATGAGGAAATGAGAACTATTCATATCTCATGCTGAGGCTGAGAAAG 660
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Db 541 GGCAGATTGATGAGGATGATGAGAACTATTCATATCTTATGCGCTGTGGAATG 600
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OY 1141 GAAGAGAAAGTGCAGGAGAGAGAGAAAGTGAAGAAAGTGAAGACCTGTTTTCAGC 1200
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Db 1081 GAGGAGAAAGTTCAGGAGAGAGAGAGAAAGTGAAGAAAGTGAAGACCTGTTTTCAGC 1134
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OY 1201 TGGATTTTCATCGGAGTTGAGAAATATGA 1230
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Db 1135 TGGATTTTCACCGTCAGATCATCATATGA 1164

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RESULT 2
US-08-471-791-15
; Sequence 15, Application US/08471791
; Patent No. 5723595
; GENERAL INFORMATION:
; APPLICANT: Thompson, Gregory A
; APPLICANT: Knaut, Vic C
; TITLE OF INVENTION: Plant Desaturases-Compositions
; TITLE OF INVENTION: and Uses
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calgene, Inc.
; STREET: 1920 Fifth Street
; CITY: Davis
; STATE: California
; COUNTRY: USA
; ZIP: 95616
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.1
; SOFTWARE: Microsoftword 5.1 (a)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,791
; FILING DATE: 6-JUNE-95
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/762,762
; FILING DATE: 16-SEPT-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/01746
; FILING DATE: 14-MAR-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/615,784
; FILING DATE: 14-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/567,373
; FILING DATE: 13-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/494,106
; FILING DATE: 16-MAR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Lassen, Elizabeth
; REGISTRATION NUMBER: 31,845
; NAME: Donna E. Scherer
; REGISTRATION NUMBER: 34,719
; NAME: Carl J. Schwedler
; REGISTRATION NUMBER: 36,924
; REFERENCE/DOCKET NUMBER: CGNE 69-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (916) 753-6313
; TELEFAX: (916) 753-1510
; TELEX: 350370 CGNE
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1668 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; US-08-471-791-15
Query Match 42.6%; Score 572; DB 1; Length 1668;
Best Local Similarity 69.1%; Pred. No. 5.4e-154;
Matches 823; Conservative 0; Mismatches 341; Indels 27; Gaps 2;
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QY 111 ACCATGACAGAGTTAGCTCTCCAAAGGTTTCATGGCTTCCACTGTCACTCTACTC 170
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 89 ACCATGGCCACTTACCAGTTCCTTAAGTTCTACATGGCTCTACCCCTCAAGCTTGTTG 148
QY 171 CATGGTCTGTATATCTCAAAAGTCC-----GCCAATCTTCAAGT 212
    || || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 149 TAGAGAACTGTAGAAATCTGACAGAGCTTTTCATGCTCTCGGAGGTTCATGTTAGGT 208
QY 213 CACTCACTCTATGACCCCAAAAGCTAGAAATATTCAAAGTCCCTGATGATTTGGGCTAG 272
    || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 209 TACCATTCTATGCCACCCCAAAAGATGATGATCTTTAAATCCCTAGACAATTTGGGCTGA 268
QY 273 GACCAATGTGTTGATTCACCTCAATCTGTCCAGAAATTTGGCAACCAAGACTACTT 332
    || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 269 GGAGAACATTTCTGGTTTCATCTCAAGCCACTGTAGAAATTTGGCAACCCAGATTTT 328
QY 333 GCCGATCCGGTGTACAGAGATGTGAGAGCAAGTGGGAGTTGAGGAAAGGGCCAA 392
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 329 GCCAGATCCCGCTCTGATGATTTGATGAGCAAGTCAGGAGACTGAGGAGAGCAAA 388
QY 393 GGAGATCCCGAGCACTATTTTGTGTGTAGTTGGAGATATGATCAGAGAAAGCACT 452
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Db 389 GGAGATTCCTGATGATTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 448
QY 453 TCCAACTATATATGCTATGCTCAATAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 512
    || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 449 TCCCACTTATCAAAACAAATGCTCAATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 508
QY 513 GCCCAGTGGTGGCAATGTGACTAGGACTGAGTGGCAAGATTAATGACATGTGTGA 572
    || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 509 TCCCTACTTCTTGGCAATTTGACAGAGGCAATGAGTGGGAGAAATGACATGTGTGA 568
QY 573 CCTTCTCAATAGTACCTTTATTTGTCTGAGAGGTTGATGAGGAAATTTGAGAGAC 632
    || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 569 CCTCTCAATAGTATTTCTTACTTATCTGAGAGTGTGACATGAGCAATTTGAGAGAC 628
QY 633 TATTTAATATCTATGCTGCTCAGAAATGATATCAAGTAGAAACGCCCTACTAGG 692
    || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 629 AATTCATATTTGATTTGTTGCTCAGAGATGATGATCAGGAGAAACGATCAATCTTGG 688
QY 693 CTTTCATCTACATGCTTCCAGAGAGACACCTTCATCCATCCCAACACACGCCAA 752
    || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 689 GTTCATCTATATCATATCTCAGAGAAAGGCAACTTCATTTCTCATGGGAGCACTGCCG 748
QY 753 GCTGGCCCAACTAGAGGCAAGAACTGCTCATCTGCGGCTCCATCCCTCCGA 812
    || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 749 ACAAGCCAAAGAGCATGTGAGACATAAAGTTGCTCAATATGTGTACATTTCTGTGAGA 808
QY 813 CGAGAAAGCCGACGCCACAGCTTACACCAAGATCTGAGAAAGCTGCTGAGATGACCC 872
    || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 809 TGAGAAAGCCCATGTAGACAGCTTACACAAAGATAGTGAAGAAACCTTTGAGATGATCC 868
QY 873 GGACACAAACAGTAATTTGCTTTGACAGATATGATGCCCAAAAAATTAACATGCCACGCA 932
    || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 869 TGATGAACTGTTTGGCTTTGCTGTGATGATGAGAAAGAAATTTCTATGCTCTCACA 928
QY 933 CTTGATGTACGAGAGAGTACTTCTTTTAAACATTTTCACGGCGTCTCTAGAG 992
    || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 929 CTTGATGTATGATGAGCGGAGATGATATCTTTTTCACACTTTTCAGCTTTTCGACGCG 988
QY 993 ACTGAGGTTTATTTGCTTGTGATTTATTCGACATCTTAGAGTTTCTGTGATTAATG 1052
    || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 989 TCTTGGAGCTTACAGAGCAAGGATTTATCAGATATATTGAGGTTCTGTGGGCGAGATG 1048
QY 1053 GAATGTGAGAAAGCTTAGGGGCTGTGAGAGAGGGGCAAAAGGCCCAAGATATGATG 1112
    || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1049 GAAAGTGGATTAACCTTAGCGGCTTTCACCTGAGGAGCAAAAGCTCAGAGACTATGTTG 1108
QY 1113 TGAATTTGGTCCCAAGATTTAGGCGAGTGTGAGAGAAAGTGCAGGGAGAGAGAAAGAA 1172
    || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1109 TCGGTTTACTCCAGAAATTTAGAAAGGCTGGAAGAGAGAGCTCAAGAGAAAGGCAAG----- 1163
QY 1173 GAAAGCTGAGCAACCTGTTTCTTTCAGCTGATTTTCAATCGGAGCTTCAAGATATGAA 1232
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Db 1164 -----GAAGCACCCACCATGCTTTCAGCTGATTTTGTGATAGGCAAGCTGTAGGT 1219
QY 1233 AGGAGGAGAGAGGAATGAGAGACCAATGAGTGTAGATTTCTATATATCC 1283
    || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1220 GCCTAAAGTGCAGACCAACCAAGATGTAGTTTCATCTTTTCATATGC 1270

RESULT 3
US-08-926-522-3
; Sequence 3, Application US/08926522
; Patent No. 6426447
; GENERAL INFORMATION:
; APPLICANT: Vic C. Knauf
; APPLICANT: Gregory A. Thompson
; TITLE OF INVENTION: PLANT SEED OILS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calgene, Inc.
; STREET: 1920 Fifth Street
; CITY: Davis
; STATE: CA
; COUNTRY: USA
ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: Microsoft Word 5.1(e)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/926,522
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/458,173
FILING DATE: 2-June-1995
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth Lassen
REGISTRATION NUMBER: 31,845
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: CGNE DES
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1668 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
US-08-926-522-3

Query Match 42.6%; Score 572; DB 4; Length 1668;
Best Local Similarity 69.1%; Pred. No. 5,4e-154;
Matches 823; Conservative 0; Mismatches 341; Indels 27; Gaps 2;
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Db 1141 TTGACCGGCTATCTGTTGAGGCGCTAAAGCCAGATTATGTTGCGGTTGCCACCA 1200
Qy 1126 AAGATTAGCGAGTGGAGAGAGTGCAGGGGAGAGAGAGAAAGATGAGAC 1185
Db 1201 AGAATAGAGAGGCTGAGAGAGAGCTCAGGCGAGCAAG-----GAAGGACT 1251
Qy 1186 CCGTTCTTTCAGCTGATTTTCATCGGAGTTGAGATGAAACAGAGGGAAG 1244
Db 1252 GTTGTTCATTGCTGATTTTCGATAGACAGCTGTAAGCTGTAAGAAAAAAGCG 1310

RESULT 8

US-08-926-522-1
; Sequence 1, Application US/08926522
; Patent No. 6426447
; GENERAL INFORMATION:
; APPLICANT: Vic C. Knauf
; APPLICANT: Gregory A. Thompson
; TITLE OF INVENTION: PLANT SEED OILS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calgene, Inc.
; STREET: 1920 Fifth Street
; CITY: Davis
; STATE: CA
; COUNTRY: USA
; ZIP: 95616
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.1
; SOFTWARE: Microsoft Word 5.1(a)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/926,522
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/458,173
; FILING DATE: 2-June-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth Lassen
; REGISTRATION NUMBER: 31,845
; NAME: Donna E. Scheret
; REGISTRATION NUMBER: 34,719
; NAME: Carl J. Schwedler
; REGISTRATION NUMBER: 36,924
; REFERENCE/DOCKET NUMBER: CGNE DES
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (916) 753-6313
; TELEFAX: (916) 753-6313
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1533 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
US-08-926-522-1

Query Match 38.8%; Score 522; DB 4; Length 1533;
Best Local Similarity 68.5%; Pred. No. 1.1e-139;
Matches 739; Conservative 0; Mismatches 331; Indels 9; Gaps 1;

Qy 166 AACCTCATGTTCTTATATCTCAAAAGTCCGCCAAATCTTCAAGTCACTCATATG 225
Db 241 AATGCCAAAGGCTTTTAACTCCACAGAGAGTTTCATGTTAGGAGCACTCCATG 300
Qy 226 CCACCCCAAAAGCTAAGATATTCAGTCCCTGATGATGGGCTAGAACATATGTTG 285
Db 301 CCACCCCAAAAGATATGAGATTTTCAATTCATGAGGAGGTTGGGCTAGCAACATATTTG 360
Qy 286 ATTCACTCAAAATCTGTGAGAAATCTTGGCAACCAACAGACTTACCTGCCGATCCGGTG 345

Db 361 GTTACCTAAAGCCAGTGGAGAAATGTTGGCAACCAAGAGATTTCTTCCGGACCTCGCA 420
Qy 346 TCAGACGATTCGAGAGAGACCTCGGAGTGTGAGAGAGGCGCAAGGATTCGCCGAC 405
Db 421 TCTGAAAGATTTGATGACAAATGCAAGAACTTAAGGCGCAAGAGAGATTCCTGAT 480
Qy 406 GACTATTTTGTGTGTTAGTTGAGATATGATCAAGAGAGAGCACTTCCAAATATATG 465
Db 481 GATTACTTGTGTTTGTGTTGATATGATTTACAGAGAGAGGCTTACCTACTTACCAA 540
Qy 466 TCTATGCTCAATAGTGTGATGTTAAGATGAGACTGGGGCTGAGCCAGTCTGG 525
Db 541 ACAATGCTTAATACCTAGATGTTGTTAGTATGAGACTGGGGCTTACCTTACCCCTGG 600
Qy 526 GCAATGAGACTGAGGAGTGGAGTGGAGAGAGAAATGACATGGTGGCTTCATATAG 585
Db 601 GCTGTCTGACTAGGCTTGGAGCTGAAAGAGACAGGCTGGGATCTTCTCCACACC 660
Qy 586 TACCTTATTTGTTCTGAGAGGTTGATATGAGAAATGAGAACTATTCATATCTC 645
Db 661 TATCTTACCTTTCTGGGCGGTAGACATGAGGAGATACAGAAATTCATCTACTC 720
Qy 646 ATGCGCTCAGGAATGATATCAAGTCAAGAAACAGCCCTTACTAGGCTTCATCTACCA 705
Db 721 ATTGGGTCAAGAAATGATCTCGTACCAAAACAGCCCTTACTTGGGTTCTATCTACCA 780
Qy 706 TCCCTCCAGAGAGACACCTTCATATCCATGCCAAGACAGCAAGCTGGCCCAAC 765
Db 781 TCGTTTCAAGAGCTGCGACATTTGTTCTACAGAAACCGCGAGGATGCAAAAGAT 840
Qy 766 TAGGCGCAAGAACTCTGCTACATCTGCGGCTCCATCGCTCCGACAGAAAGCGCAC 825
Db 841 CATGGGAGACGTGAAGCTGGGCGCAATTTGTGTCAATCGGTCTGACGAAGACGTAC 900
Qy 826 GCCACAGCCTACACCAAGATCTGGAAGAGCTGCTAGATCGACCCGACACAACGTA 885
Db 901 GAGACCGCTTATACAAAGATATGCGAAAGCTATTCGAGATCGATGCGACCGTT 960
Qy 886 ATTGCTTTGAGATATGATGCGCAAAATAACATATGCGAGGCACTTGATATGACG 945
Db 961 CTGCTTTTCCGACATGATGAGAAAGATCTCGATGCCCGCACCTTGATATGAT 1020
Qy 946 GGAAGTGCAGCACTCTTTTAAACATTTCAAGCGGCTGCTCAGAGAGTNGGTTAT 1005
Db 1021 TGGGCTGATGACAACTCTTGAACATTTCTCGGCGGTGGCCAAAGATCGGCTTAC 1080
Qy 1006 TCTGCTTGATTTATTCGACATCTTAGAGTTTCTGTTGATTAATGATGTGGAAG 1065
Db 1081 ACCGCCAAAGACTACGCCGACATACGTGAATTTCTGTCGGGCGTGAAGAGTGGCGAT 1140
Qy 1066 CTTACGGGGCTGTGCGAGGCGGCGAAAGCGGAGAAATATGTTGATTTGGTCCG 1125
Db 1141 TTGACCGGCTATCTGCTGAGAGGCTTAAGCCGCAATTAATGTTTCCGGTTCACCA 1200
Qy 1126 AAGATTAGGCGAGTGAAGAGAAAGTGCAGGGGAGAGAGAGAAAGAAAGCTGAGCAC 1185
Db 1201 AGAATCAGAGGCTGAGAGAGAGCTCAAGGGCGACCAAG-----GAAGGACT 1251
Qy 1186 CCGTTCTTTCAGCTGATTTTCATCGGAGTTGAGATGAAACAGAGGGAAG 1244
Db 1252 GTTGTTCATTGCTGATTTTCGATAGACAGCTGTAAGCTGTAAGAAAAAAGCG 1310

RESULT 9

PCT-US91-01746-12
; Sequence 12, Application PC/TUS9101746
; GENERAL INFORMATION:
; APPLICANT: Thompson, Gregory A
; APPLICANT: Knauf, Vic C
; TITLE OF INVENTION: Plant Desaturases-Compositions and Uses
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:


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ORIGINAL SOURCE:
ORGANISM: glycine max
STRAIN: Cultivar Wye
DEVELOPMENTAL STAGE: Developing seeds
IMMEDIATE SOURCE:
LIBRARY: cDNA to mRNA
CLONE: pDS1
FEATURE:
NAME/KEY: 5' non-coding sequence
LOCATION: 1..69
OTHER INFORMATION: /note= "IDENTIFICATION
METHOD=deduced by proximity to location 70-72"
FEATURE:
NAME/KEY: Putative translation initiation codon
LOCATION: 70..72
OTHER INFORMATION: /note= "IDENTIFICATION
METHOD=Similarity of the context of the
OTHER INFORMATION: methionine codon in the open reading frame to
OTHER INFORMATION: translation
FEATURE:
NAME/KEY: Putative transit peptide coding sequence
LOCATION: 70..165
OTHER INFORMATION: /note= "IDENTIFICATION
METHOD=deduced by proximity to location 70-72"
OTHER INFORMATION: and location 166-1242"
FEATURE:
NAME/KEY: Mature protein coding sequence
LOCATION: 166..1242
OTHER INFORMATION: /note= "IDENTIFICATION
OTHER INFORMATION: METHOD=Experimental determination of N-terminal
OTHER INFORMATION: amino acid sequence and subunit size of
OTHER INFORMATION: purified soybean
FEATURE:
NAME/KEY: Translation termination codon
LOCATION: 1243..1245
OTHER INFORMATION: /note= "IDENTIFICATION
OTHER INFORMATION: METHOD=The translation codon ends the open
OTHER INFORMATION: reading frame for a protein of the expected
OTHER INFORMATION: size"
FEATURE:
NAME/KEY: 3' non-coding sequence
LOCATION: 1246..2243
OTHER INFORMATION: /note= "IDENTIFICATION
OTHER INFORMATION: METHOD=Established by proximity to location
OTHER INFORMATION: 1243-1245"
US-07-995-657-1
Query Match 38.8%; Score 521.2; DB 1; Length 2243;
Best Local Similarity 68.5%; Pred. No. 2.2e-139;
Matches 743; Conservative 0; Mismatches 324; Indels 18; Gaps 1;
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Db 418 GAGATTCCAGATGATTTACTTTGTTGTTCTGTGCGACATGATTCACAGAGAAAGCTCTG 477
Qy 454 CCACATATATATGTCATGCTCAATAGGTGATGATTAATTAAGATGAGACTGGGGCTGAG 513
Db 478 CTTACTTACCAACTATATGTTAAATACTTTGATGAGAGTGTGATGAACAGGTGGCAGC 537
Qy 514 CCGAGTCTTGGGCAANTGTGACTAGGGCATGAGCTCCGACAGAAATTAACATGTTGAC 573
Db 538 CTTACTTCCCTGGGCAATTTTGGACAGGGCAGTGAAGCTGCTAAGAAACACAGCGGTGAT 597
Qy 574 CTTCTCAATATAGTACCTTTATTTGTGGAAGGGTTGATATGAGAAATTTGAAGACT 633
Db 598 CTTCTTACCAATATCTGATCTTGATGAGAGAGTGTACATGAACAATTTGAAGACACA 657
Qy 634 ATTCAATATCTCATCGGCTCAGGAGATGATATCAAGTCAGAAAAACAGCCCTCAAGGC 693
Db 658 ATTACAGTACCTTATTTGGTGTGGATGATGATCTCGACAGCAAGAACCCCTACCTTGGT 717
Qy 694 TTGATCTACACATCTTTCCAGAGAGAGCAACCTTCATATCCCATGCGCAACAGCCAG 753
Db 718 TTGATTTACACTTCATTTTCAAGAGAGGGCAACCTTCATATCCCAAGAAACAGCGCGAG 777
Qy 754 CTGGCCCAACTAGCGGCGCAAGAACCTTCACATCTGCGGCTGCATGCGCTCCGAC 813
Db 778 CTTGCGAAGAGAGCATGATGATTAATTAATTTGACAGATCTGCGCATGATTCCTCATGAT 837
Qy 814 GAGAGAGCCACGACGACAGGCTACACCAAGATGCTGGAAGAGCTCGCTGAGATGAGACCC 873
Db 838 GAGAGAGGCGCAGAGACTGCATACACAAAGATAGTGAAGAGCTGTTGAGGTTGATCT 897
Qy 874 GACACACAGTAAATGCTTTTGCAGATATGATGCGCAAAAAATTAACATGCCAGCCAC 933
Db 898 GATGCTACAGTATGAGCATTTTGGCGACATGATGAGAAAGATTTGCTATGCCAGCACAC 957
Qy 934 TTGATGAGAGGGAAGTGAAGCACTTTTAAACATTTACGCGGGTGTGCACAGA 993
Db 958 CTTATGATATACCGCCCGCGAGACACCTGTTGATTACTACTGTCGCGGCGACAGCGC 1017
Qy 994 GTGNGGTTTATTTCTGCGTTGATTTAGGACATCTTTAGAGTTCTGTGATTAATG 1053
Db 1018 ATTGGGTTCTACACTGCAAGAGACTATGCTGACATCTGCAATTTCTGTGGGAGGTGG 1077
Qy 1054 AATGTGAAGGCTTACGGGCTGTGCGAGAGGGGGAAGCGCAGAAATATGTGTG 1113
Db 1078 AAGGTGAGCAGCTAACCGGACCTTTCAGTGAGGGAAGAAAGGCTCAGGATACGTTGT 1137
Qy 1114 GAATGGGTCGCCAAGATTAGCGAGTGAAGAGAAAGTGCAGGGGGAAGGAAGCAAG 1173
Db 1138 GGGCTGCGACCAAGAAATCAGAAGGTTGGAGAGAGAGCTCAAGCAAGAGCAAGAGTGG 1197
Qy 1174 AAAGC 1178
Db 1198 TCAGC 1202
RESULT 12
US-08-474-587-1
; Sequence 1, Application US/08474587
; Patent No. 5760206
; GENERAL INFORMATION:
; APPLICANT: Hitz, William D.
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Perez-Grau, Luis
; TITLE OF INVENTION: Nucleotide sequence of
; Patent No. 5760206
; TITLE OF INVENTION: Soybean Stearoyl-ACP
; NUMBER OF INVENTIONS: 12
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: E. I. du Pont de Nemours
; AND COMPANY
; STREET: 1007 Market Street
; CITY: Wilmington
```

STATE: Delaware
 COUNTRY: U.S.A.
 ZIP: 19898
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
 COMPUTER: Macintosh
 OPERATING SYSTEM: Macintosh System, 6.0
 SOFTWARE: Microsoft Word, 4.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/474,587
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: SIEGEL, BARBARA C.
 REGISTRATION NUMBER: 30,684
 REFERENCE/DOCKET NUMBER: BB_1022-C
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 302-992-4931
 TELEFAX: 302-773-0164
 TELEX: 835420
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2243 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Glycine max
 STRAIN: Cultivar Wye
 DEVELOPMENTAL STAGE: Developing seeds
 IMMEDIATE SOURCE:
 LIBRARY: cDNA to mRNA
 CLONE: pDS1
 FEATURE:
 NAME/KEY: 5' non-coding sequence
 LOCATION: 1..69
 OTHER INFORMATION: /note="IDENTIFICATION
 METHOD-deduced by proximity
 OTHER INFORMATION: to location 70-72"
 FEATURE:
 NAME/KEY: Putative translation initiation codon
 LOCATION: 70..72
 OTHER INFORMATION: /note="IDENTIFICATION
 METHOD-similarity of the
 OTHER INFORMATION: context of the methionine
 OTHER INFORMATION: codon in the open reading frame to translation
 FEATURE:
 NAME/KEY: Putative translt peptide coding sequence
 LOCATION: 70..165
 OTHER INFORMATION: /note="IDENTIFICATION
 METHOD-deduced by proximity
 OTHER INFORMATION: to location 70-72 and
 OTHER INFORMATION: location 166-1242"
 FEATURE:
 NAME/KEY: Mature protein coding sequence
 LOCATION: 166..1242
 OTHER INFORMATION: /note="IDENTIFICATION
 METHOD-experimental
 OTHER INFORMATION: determination of N-terminal
 OTHER INFORMATION: amino acid sequence and subunit size of purified soybean
 FEATURE:
 NAME/KEY: Translation termination codon
 LOCATION: 1243..1245
 OTHER INFORMATION: /note="IDENTIFICATION
 METHOD=the translation
 OTHER INFORMATION: codon ends the open reading
 OTHER INFORMATION: frame for a protein of the expected size"

FEATURE:
 NAME/KEY: 3' non-coding sequence
 LOCATION: 1246..2243
 OTHER INFORMATION: /note="IDENTIFICATION
 METHOD=Established by
 OTHER INFORMATION: proximity to location
 OTHER INFORMATION: 1243-1245"
 US-08-474-587-1
 Query Match 38.8%; Score 521.2; DB 1; Length 2243;
 Best Local Similarity 68.5%; Pred. No. 2,2e-139;
 Matches 743; Conservatve 0; Mismatches 324; Indels 18; Gaps 1;
 QY 112 CCAAGTACCAAGAGTTAGCTCCAGGGTTTCAAGGCTTCCACTGCACTAAGTCC 171
 DB 118 CAATGCCAGCGCCAGATGCTCCCGCTCCGATGCTCCACCTCCGCTCGGTCC 177
 QY 172 ATGGTTTATATATCAAAAGCCGCCAA-----ATCTCAAGTC 213
 DB 178 AAGAGGTTGAATATTAAGAGCCATTCCTCCAGAGAGTGCATGTTCAAGTA 237
 QY 214 ACTCACTATAGCCACCCCAAAAGCTAGAAATATTCAGTCCCTTGATGATGGGCTAGG 273
 DB 238 ACCGACGCTATGCTCCGCCAGAGATGAGATTTTCAATCTTGGAGATGGGCTGAC 297
 QY 274 AACATGTGTTGATTCACCTCAAAATCTGCGAATAATCTTGGACACCAAGACTACTTG 333
 DB 298 CAGAACATCTTGACTCATCTTAAACCTGTAGAAAAATGTTGGCAACCAAGAGATTTTGA 357
 QY 334 CCGGATCCGGTGTGACAGGAGATTCGAGAGCAAGTGGGAGTTGAGAGGAAAGGCCAAG 393
 DB 358 CCGGACCCCTCTCGATGATGATTAAGAGCAAGTGAAGAACTGAGAGAGAGGCAAG 417
 QY 394 GAGATTCGCCAGAGACTATTTTGTGTGTTAGTTGAGATATGATCAGAGAAAGCACTT 453
 DB 418 GAGATTCAGATGATTAATCTTGTGTTCTTGCGGAAACATGATCAGAGAGAAAGCTGTG 477
 QY 454 CCAACATATATGCTATGCTCAATAGGTGATGATTAAGATGAGACTGGGCTGAG 513
 DB 478 CTTACTTACCAAACTATGTTAAATCTTGTGATGAGATTCGTGTGAAACAGGCTCCAGC 537
 QY 514 CCGAGTCTTGGGCAATAGTGCATGAGGCAATGAGCTCCGGAAGAAATAGACATGAGTGC 573
 DB 538 CTTACTCTCGGGCAATTTTGAACAAGGCAATGAGCTCTTAAGAAACACACACGGTGTAT 597
 QY 574 CTTCTCAATAGTACCTTTATTTGTCGGAAGGTTGATATGAGAAATTGAAGACT 633
 DB 598 CTTCTTAACAATATATGCTGATGAGTGAAGATGATGATGAACAATTTGAAGAGACA 657
 QY 634 ATTCAATATCTCATGCGCTCAGGAATGATATCAAGTCAGAAACAGCCCTTACCTTAGGC 693
 DB 658 ATTCACTACCTTATTTGGGTCGGAATGATGATTCGAGCCAGAAACAGCCCTTACCTTAGGT 717
 QY 694 TTCACTACACATCTTCCAGAGAGAGCAACCTTCATATCCCATGCAACACAGCAAG 753
 DB 718 TTATTTTACCTTATTTTCAAGAGAGGCAACCTTCTATATCCACGAAACAGGCCAGG 777
 QY 754 CTGGCCCAACACTAGCGCGCAAGAAACCTGCTCAATCTGCGCTCCATCAGCCCTCGAC 813
 DB 778 CTGCGAAGAGAGATGATGATTAATAATTTGSCAGATGCTGCGCATGATTTGCTCGAT 837
 QY 814 GAGAACGGCCAGCCAGAGCTTACACCAAGATGTGGAAGAAAGTCCGTAGATGACACC 873
 DB 838 GAAACACGGCCAGCAAGCTGATACAAAAATAGTGAAGAAAGCTGTTTGAAGTTGATCTT 897
 QY 874 GAGACACAGATATTCCTTTTGCAGATATGATCGCAAAAAAATAACAATGACGAGGCA 933
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 QY 934 TTGATGTACGACGAGAGTACGAACTTTTAAACATTTACGGCGGTTGCTCAGAGA 993
 DB 958 CTTATGTATAGAGGGCGGCGAGCAACCTGTTTGAATACACTCTGCGGCGGAGCGG 1017


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US-08-926-522-5
; Sequence 5, Application US/08926522
; Patent No. 6426447
; GENERAL INFORMATION:
; APPLICANT: Vic C. Knaf
; APPLICANT: Gregory A. Thompson
; TITLE OF INVENTION: PLANT SEED OILS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calgene, Inc.
; STREET: 1920 Fifth Street
; CITY: Davis
; STATE: CA
; COUNTRY: USA
; ZIP: 95616
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.1
; SOFTWARE: Microsoft Word 5.1(a)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/926,522
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/458,173
; FILING DATE: 2-June-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth Lassen
; REGISTRATION NUMBER: 31,845
; NAME: Donna E. Scherer
; REGISTRATION NUMBER: 34,719
; NAME: Carl J. Schwedler
; REGISTRATION NUMBER: 36,924
; REFERENCE/DOCKET NUMBER: CGNE DES
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (916) 753-6313
; TELEFAX: (916) 753-1510
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1495 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; US-08-926-522-5

```

```

Query Match      38.1%; Score 511.8; DB 4; Length 1495;
Best Local Similarity 69.3%; Pred. No. 8.8e-137;
Matches 715; Conservative 0; Mismatches 308; Indels 9; Gaps 1;
QY 206 TTCACGCTACCTACCTATGACCCCAAAAGCTAGCAATATTCAGTCCCTGATGATT 265
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 251 TTCACGCTACCTACCTATGACCCCAAAAGCTAGCAATATTCAGTCCCTGATGATT 310
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 266 GGGCTAGCAACAAATGTTGATTACCTCAATCTGTGAGAAATCTTGGCAACACAG 325
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 311 GGGCCGAGCACTTCTAAGTACAGTCAAAAGACGTGAGAAAGTGTGGACGCCAGC 370
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 326 ACTACTTGGCGGATCCGGTGTGACAGCGATTCAGAGACGATGCGGAGTTGAGGAAA 385
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 371 ACTTCTTACCCGACCTGTGATCGATGGGTTCGAAAGATCAGATTAGAGACTAAGAGA 430
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 386 GGGCAAGAGATTTCCGACGATATTTTGTGTTAGTTGAGATATATCAGACAGAG 445
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 431 GGGCAAGAGAGCTCCCTGATGATTACTGCTTCTGTTGTTGGGAGACATATATCAGAG 490
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 446 AAGCACTTCCAAATATATGCTATATGCTCAATAGTGTGATGTTATTAAGATGAGACTG 505
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 491 AGGCGCTTCCGACCTATCAAAACATGTTGAAACACTTTGATGAGTGAAGGATGAAGCTG 550
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 506 GGGCTAAGCCCAATGCTTGGGCAATGTTGACTAGGCTAGGACTGCCGAAGATATGAC 565
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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DB 551 GCGCTAAGCCCACTTCAATGGGCTATTTTGACACAGAGCTTGGACTGCGAAGACACCGAC 610
QY 566 ATGCTGACCTTTCATATAGTACCTTATTTGTCTGGAAGGTTGATATGAGAAATTTG 625
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 611 ACGGTGATCTTTCATATAGATCTTACTTGTTCTGTGACGCTGATGATGAGGAGATTG 670
QY 626 AGAAGACTATTCATATGCTGAGGCTCAGAGATGATATTCAGTCAAGAAACAGCCCT 685
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 671 AAAAGACATTCAGTACTTATGTTGTTCTGAAATGATCCTAGAACAGAACAAATCCTT 730
QY 686 ACCGAGGCTTCATCTACATACATCCCTTCCAGAGAGAGACCTTATATCCATCCACACA 745
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 731 ACCCTGCTTATCTATACATCTTCCAGAGAGAGAGACCTTATCTCTCAGGAAACA 790
QY 746 CAGCCAAAGCTGGCCCAACACTAGCGGCGACAAGAACTCTGCTACATCTGCGGCTCATCG 805
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 791 CAGCTGCCCAAGCCAAAGAGAGAGAGAGACCTCAAGCTAGGCCAAATCTGGGCGCAATAG 850
QY 806 CTTCCGACGAGAAAGCGCCACAGCCCTACACCAAGATCTGTGAAAGCTGCTGAGA 865
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 851 CTGCGACGAGAAAGCGCTATGAGACAGCTTACACCAAGATAGTTGAGAAAGCTCTTGAGA 910
QY 866 TCGACCCCGACACACAGTAAATGCTTTTGAGATATGATCGCGAATAAATATACATTC 925
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 911 TTGATCTGATGTTAGTGTGATGAGGCTTTGCGACATGATGAGAGAAATCTCGATTC 970
QY 926 CAGCGCACTTGAATGATGACGAGGAGAGTACGAACTTTTAAACATTTTCACGCGGTTG 985
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 971 CTGCTCACTTGAATGATGATGAGGAGGAGATGAAGCCCTTTGACAACTTCTCTTCTTG 1030
QY 986 CTCAGAGAGTGNNGGTTTATTTCTGCTTGTGATTTATTCGACATCTTGAAGTTCTGTGG 1045
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1031 CTCAGAGAGTGNNGGTTTATTTCTGCTTGTGATTTATTCGACATCTTGAAGTTCTGTGG 1090
QY 1046 ATAAATGGAATGGAAGAGGCTTACGGGCTGTGCGACAGAGGGGCGAAGCCGAGAAAT 1105
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1091 GGAAGTGAAGATTTGAGAGCTTTCGCGGCTTTTCAGGTGAAGAAACAAAGCCGAAAGT 1150
QY 1106 ATGCTGTGAATTTGGTCCCAAGATTTAGCGGAGTGTGAAGAAAGTGCAGGGAGAGAGA 1165
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1151 ACTTGTGTGGTTGATCTCAAGATTCAGAGGTTGATGATGAGAGCTCAAGCAAGAGACCA 1210
QY 1166 AGAAGAAAGAAAGCTGACACCCCTGTTTCTTCACTGATGATTTTCAATTCGAGTTGAAGA 1225
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1211 AGAA-----AGGACCCCAAGGTTCTTTCAGCTGATATCATGACAGAGAAAGTGCAGC 1261
QY 1226 TATGAACAGGAA 1237
    ||||| ||||| |||||
DB 1262 TCTAAAAAGGAA 1273

```

Search completed: December 2, 2002, 00:41:48
Job time : 84 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 1, 2002, 21:12:16 ; Search time 304 Seconds

(without alignments)
9956.203 Million cell updates/sec

Title: US-09-732-597-1

Perfect score: 1344

Sequence: 1 caaccgccagaataataaat.....ttgagtttaagtaaaaa 1344

Scoring table:
IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_101002:*
1: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
2: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
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4: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
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21: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	613.4	45.6	1309	AA092889	Coriander omega-12
2	573.8	42.7	1643	AA035667	DNA encoding a ste
3	572	42.6	1668	AA015252	Ricinus communis d
4	568.8	42.3	1668	AA013964	R. communis delta9
5	555.8	41.4	1092	AA084531	Mature castor enzy
6	522	38.8	1533	AA013963	C. tinctorius delt
7	522	38.8	1533	AA022616	Carthamus tinctori
8	522	38.8	1533	AA064003	Sequence encoding
9	522	38.8	1533	AA015250	Carthamus tinctori

10	522	38.8	1533	20	AA035666	DNA encoding a ste
11	521.6	38.8	1524	15	AA055760	Delta-9-desaturase
12	521.4	38.8	1529	18	AA063437	Rapeseed stearyl-
13	521.2	38.8	2243	13	AA020187	Soybean seed stea
14	521.2	38.8	2243	19	AA029236	Nucleotide sequenc
15	516.4	38.4	1553	22	AA022378	Cotton stearyl-AC
16	514.6	38.3	1683	18	AA063438	Rapeseed stearyl-
17	513.6	38.2	1714	21	AA035179	Corn delta-9 stea
18	513.2	38.2	1176	16	AA000397	Stearyl-ACP-desat
19	513.2	38.2	1206	24	ABA94566	A. thaliana fatty
20	513.2	38.2	1342	21	AA042392	Stearyl-ACP-desat
21	513.2	38.2	1552	16	AA000396	Stearyl-ACP-desat
22	513.2	38.2	1687	21	AA048442	Arabidopsis thalia
23	513.2	38.2	1689	21	AA039517	Arabidopsis thalia
24	513.2	38.2	2243	16	AA000395	Stearyl-ACP-desat
25	513	38.2	1107	21	AA061031	Nucleotide sequenc
26	513	38.2	1621	18	AA062127	Zea mays delta-9 d
27	513	38.2	1621	21	AA061026	Nucleotide sequenc
28	511.8	38.1	1495	12	AA013965	B. campestris delt
29	511.8	38.1	1495	19	AA015253	Brassica campestr
30	509.4	37.9	1080	16	AA000398	Mature stearyl-AC
31	498.8	37.1	1567	21	AA037983	Arabidopsis thalia
32	495.8	36.9	1651	21	AA037494	Arabidopsis thalia
33	489.6	36.4	1709	21	AA035180	Corn delta-9 stea
34	483.4	36.0	1667	17	AA027645	Delta-9-fatty acid
35	428.8	31.9	2751	22	ABA94565	A. thaliana fatty
36	426.6	31.7	2751	24	AA050960	Plastidial delta 9
37	426.4	31.7	1272	20	AA081284	DNA encoding delta
38	415	30.9	1395	21	AA035393	Arabidopsis thalia
39	393.8	29.3	1258	17	AA018906	Delta-6-palmitoyl
40	392.4	29.2	1560	24	AA032889	Soybean diverged d
41	367.6	27.4	1318	24	AA032906	Rice diverged delt
42	362.6	27.0	1415	24	AA032904	Corn diverged delt
43	334.6	24.9	1717	24	AA029242	Plasmaid pB68 2X E
44	303	22.5	1234	21	AA053615	Arabidopsis thalia
45	284.6	21.2	2705	19	AA031999	Flax SMD2 gene. L

ALIGNMENTS

RESULT 1
AA092889 standard; cDNA: 1309 BP.
ID AA092889:
XX
AC AA092889:
XX
DP 05-DEC-1995 (first entry)
XX
XX
DE Coriander omega-12 desaturase cDNA.
XX
KM Coriander; omega-12 desaturase; petroselinic acid;
KW transgenic plant; crop improvement; tobacco; ss.
XX
XX
OS Coriandrum sativum.
XX
XX
FH Key
FT CDS
FT
FT sig_peptide
FT
FT
FT mat_peptide
FT
FT
XX US5430134-A.
XX PN
XX PD
XX 04-JUL-1995.
XX PF
XX 07-AUG-1992; 92US-0926788.
XX PR
XX 07-AUG-1992; 92US-0926788.

```
XX (UMMS ) UNIV MICHIGAN STATE.
PA
XX
XX Cahoon EB, Ohlrogge JB, Shanklin J, Somerville CR;
XX
XX WPI; 1995-253884/33.
DR
XX P-PSDB; AAR76578.
XX
XX New omega-12 desaturase from coriander - and DNA encoding it, useful
XX for making transgenic plants able to synthesise petroselinic acid.
XX
XX Disclosure; Columns 17-18; 25pp; English.
XX
XX A cDNA library prep'd. from developing seeds of coriander was
XX screened with a probe based on a partial cDNA clone (AA092888) of
XX omega-12 desaturase to isolate full-length clone EC201 (AA092889).
XX Expression of this cDNA in transgenic tobacco callus resulted in
XX prodn. of petroselinic acid (18:1 omega 12) and omega-12
XX hexadecenoic acid.
XX
XX
XX Sequence 1309 BP; 360 A; 280 C; 319 G; 350 T; 0 other;
SQ
Query Match 45.6%; Score 613.4; DB 16; Length 1309;
Best Local Similarity 77.0%; Pred. No. 2e-162;
Matches 762; Conservative 0; Mismatches 222; Indels 6; Gaps 1;
OY 241 GAAATATTCAAGTCCCTTGATGATGCGTAGAACAATGTGTGATTCACCTCAATCT 300
DB 181 GAAATGTTCAACTCTCTGAGAGGTTGGCCAGGACACATCTTGTGACCTGMAATCC 240
OY 301 TCGAGAAATCTTGGACACACAGACTACTCTGCGGATCCGCTGTGACAGGATTCGAG 360
DB 241 GTAGAGAACTCATGCGACCGCAAGACTATCTGCCCATCCCACTCCATGATTTGAA 300
OY 361 GAGCAAGTCGGGAGTTGGAGGAAAGGCCAAGGATTCGCCAGCACTATTTGGGTG 420
DB 301 GATCAAGTCAAGAGATGAGAGAGAGCGCCAGACATCTCTGATGAATCTTGTGTT 360
OY 421 TTAGTTGAGATATGATCAGAGAAAGCACTTCCAACTATATCTCTATGCTCAATAG 480
DB 361 CTGTGGAGACATGATCATCTGAGAGGCACTCCAACTACATGCTATGCTTAAACAGA 420
OY 481 TGTGATGATTTAAGATGAGACTGGGGCTGAGCCCACTGCTTGGGCAATGTGACTAG 540
DB 421 TGTGATGGCATTTAAGATGAGACTGCGCTCAACTCTTCTTGGCCACTTGGACAG 480
OY 541 GCATGACATGCCGAAGATGAGATGATGACCTTCTCAATAGTAACCTTATTTGCT 600
DB 481 GCTTGAGACTGCTGAGAGAAACCGCATGGGCACTTCTCAACAAGATATCTTATCTCT 540
OY 601 GGAAGGGTTGATATGAGAAATTTGAGAAAGACTATTCATATCTCATCGCTCAGCAATG 660
DB 541 GCGCGAGTTGATATGAGATGATGAGAAAGACTATTCATATCTCATCGCTCAGCAATG 600
OY 661 GATATTAAGTCAGAAAACAGCCCTTACAGGCTTTCATACACATCTTCCAAAGAGA 720
DB 601 GATPACAAAACAGAGAACTGTCCTACATGAGGCTTCATACACATCTTTCAGGAAGA 660
OY 721 GGAACCTTATATCCATCCACACACAGCAAGCTGGCCCAACACATPACGGCGCAAGAC 780
DB 661 GCCACATTCATCTCCATCGCAACACAGCAAACTTGCTCAACATNCGGTGACAAAGAC 720
OY 781 CTCGCTACATCTGCGGCTCCATGCGCTCCGACGAGAGAGCCACAGCCATACACC 840
DB 721 CTAGCTCAAGTGTGGCAACATGCTTCTGACGAGAAACGCCATGCGACCGCTTACACC 780
OY 841 AAGATGTGAAAAGCTCGCTGAGATGACCCGACACAAACGTAATGTTGTTTGCAGAT 900
DB 781 AAAATGTGAGAGAGCTTGGGAGATTGACCCAGACACCACTGTATCGGATTTTGCAG 840
OY 901 ATGATGCGCAAAAATTAACATATGCGCAGCGCACTTGATGACGAGCAAGTCAAGACTT 960
DB 841 ATGATGAGGAAAGAAATPACAAATGCGACGATCATGCAATGATGATGCGATGATATG 900
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```
OY 961 CTTTAAACATTTACAGCGGTTGCTCAGAGAGTGNGGTTTATTCGCTTGATTA 1020
DB 901 CTTTAAACATTTACAGCGGTTGCTCAGAGAGTGNGGTTTATTCGCTTGATTA 960
OY 1021 TCGGACATCTTAAAGTTTCTGTGTGATTAATGATGTAAGGCTTACGGGCTGTG 1080
DB 961 TCGGACATCTTAAAGTTTCTGTGTGATTAATGATGTAAGGCTTACGGGCTGTG 1020
OY 1081 GAGCAGGCGGAAAGCGCAGCAATATGCTGAATTTGGGCTCCCAAGATTAGCGAGTG 1140
DB 1021 GGTGAAGGAGAAAGCTCAGCAATATGTTGAGCTTGCTCTAAGATCAGGAAGTT 1080
OY 1141 GAGAGAAAGTGCAGGAGGAGAGAAAGAAAGAAAGCTGAGCACCCTGTTCTTCAAC 1200
DB 1081 GAGAGAAAGTGCAGGAGGAGAGAAAGAAAGAAAGCTGAGCACCCTGTTCTTCAAC 1134
OY 1201 TGGATTTTCAATGGAGATTTGAAGATATGA 1230
DB 1135 TGGATTTTCAATGGAGATTTGAAGATATGA 1164
```

```
RESULT 2
AAK35667
ID AAK35667 standard; DNA; 1643 BP.
XX
XX AAK35667;
AC
XX
XX 16-JUL-1999 (first entry)
DT
XX
XX DNA encoding a stearyl-acyl carrier protein desaturase.
DE
XX
XX Localised mutation; target gene: plant cell;
XX recombinogenic oligonucleobase; selective growth advantage;
XX herbicide resistance; preservation; fruit; flower; ss.
XX
XX Ricinus communis.
OS
XX
XX WO907865-A1.
PN
XX
XX 18-FEB-1999.
PD
XX
XX 05-AUG-1998; 98WO-US16267.
PR
XX
XX 05-AUG-1997; 97US-0054836.
XX
XX (KIME-) KIMERAGEN INC.
PA
XX
XX Antzen CJ, Kipp PB, Kumar R, May GD;
PI
XX
XX WPI; 1999-302251/25.
DR
XX
XX Introducing mutations into target genes in plant cells - using a
XX recombinogenic oligonucleobase comprising 2 regions homologous to a
XX target gene and an intervening mutant region
XX
XX Example 5; Page 41; 53pp; English.
XX
XX The specification describes methods for introducing localized mutations
XX into target genes in plant cells. The methods comprise using a
XX recombinogenic oligonucleobase comprising 2 regions homologous to a
XX target gene and an intervening mutant region. The methods can be used
XX to introduce localized mutations into target genes to introduce desirable
XX traits, e.g. selective growth advantage under appropriate selective
XX conditions, change in colour of plant cells growing in a callus,
XX herbicide resistance, or improved preservation of fruit or flowers.
XX They can be used in plants such as maize, wheat, rice, lettuce, potato,
XX tomato, canola, soybean or cotton cell. The present sequence represents
XX a target for the methods of the invention.
XX
XX Sequence 1643 BP; 462 A; 321 C; 383 G; 477 T; 0 other;
SQ
Query Match 42.7%; Score 573.8; DB 20; Length 1643;
```


CC plant cell during lipid accumulation. Also, oilseeds having a modified
 CC level of fatty acid saturation and oils produced from such oilseeds.
 XX
 SO Sequence 1668 BP; 464 A; 325 C; 386 G; 493 T; 0 other;

Query Match 42.68; Score 572; DB 19; Length 1668;
 Best Local Similarity 69.18; Pred. No. 1e-150;
 Matches 823; Conservative 0; Mismatches 341; Indels 27; Gaps 2;

111 ACCAGTACAGAGATTGATCTCCAAAGGCTTTCACATGCTCCATGCTCACTACTC 170
 89 ACCAATGCGCATGACCATCTCTTAAGTTCTACATGCTCACTCACTCACTGCTTC 148
 171 CATGTTCTTATATCTCAAAAGTCC-----GCCAATCTTCAAGT 212
 149 TAAGGAAGTTGAGATCTCAAGAAAGCTTTCATGCTCTCGGAGAGTACATGTTCAAGT 208
 213 CACTCACTCATGCGACCCCAAAAGCTAGAAATTTCAAGTCCCTTATGATGCTGCTAG 272
 209 TACCCATTTCTATGCGACCCCAAAAGATTGAGATCTTAAATCCCTAGACAATGGCTGA 268
 273 GAAACATGTTGATGCTCACTCAATCTGCGAAGATCTTGGCAACCAAGCTACTT 332
 269 GGAACATTTCTGTTCTATCTGAAGCCAGTTGAGAAATTTGGCAACCGAGATTTT 328
 333 GCCGATCCGGTTCAGACGATTCGAGAGCAAGTGGGAGTTGAGGAAAGGCCAA 392
 329 GCCAGATCCCGCTGATGATGATTTGATGAGCAAGTCAAGGAACTCAGGAGAGACGCAA 388
 393 GAGATTTCCGACGACTATTTTGTGTGTTAGTTGAGATATGATCAAGAAAGCACT 452
 389 GAGATTTCTGATGATATTTTGTGTTGTTGAGATGATGATTAACGGAAGACCT 448
 453 TCAACATATATGCTATGCTCAATAGTGTGATGATTAAGATGATGAGATGAGCTGGA 512
 449 TCCACTTATCAACATGCTGATGATGATGATGATGATGATGATGATGATGATGATG 508
 513 GCCAGTCTTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 572
 509 TCCACTTCTTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 568
 573 CTTTCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 632
 569 CTTTCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 628
 633 TATTCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 692
 629 AATTCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 688
 693 CTTTCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 752
 689 GTTCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 748
 753 GCTGCGCCCAAGCTAGCGGAGCAAGAACTGCTACATCTGGCGGCTCCATCGCTCGA 812
 749 ACAGCGCAAAAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 808
 813 CGAGAGCGCGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 872
 809 TGAAGAGCGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 868
 873 CGACACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 932
 869 TGAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 928
 933 CTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 992
 929 CTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 988
 993 AGTGGGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1052
 989 TCTTGGAGCTTACAGCAAGCAAGATTAATGATATATGAGTCTTGGTGGGAGATG 1048

QY 1053 GAATGTGAAAGGCTTACGGGGCTGCGACAGAGGGCGAAAGCGCAGAAATATGTGTG 1112
 1049 GAAGTGGATTAACCTAACGGGCTTTACGTAGAGGACAAAGGCTCAGACTATGTTG 1108
 QY 1113 TGAATGGGCTCCCAAGATTAGCGCAGTGAAGAGAAAGTCAAGGGAAGAAAGAA 1172
 1109 TCGGTTACCTCCCAAGAAATTAAAGGCTGAAGAGAGAGCTCAAGAGGGGCAAG----- 1163
 QY 1173 GAAAGCTGAGCACCCTGTTCTTACGCTGATTTTCAATGCGGAGTGAAGATATGAA 1232
 1164 -----GAACACCCACCATGCTTTCAGCTGATTTTCAATGCGCAGAGTGAAGCTGTAGT 1219
 QY 1233 AGAAGGGAAGGAATGAGAGGAGCAAAATGAGTATGATTTCTATATGC 1283
 1220 GGTAAAGTGACAGAGCAAGCAAAATGATGATTTTCACTCTTTTTCATGTC 1270
 DB

RESULT 4
 AA013964
 ID AA013964 standard; DNA; 1668 BP.

AC AA013964;
 DT 11-DEC-1991 (first entry)
 XX
 DE R. communis delta9 desaturase from pCGN3230.
 XX
 KW Desaturase; probe; ss.
 OS Ricinus communis.

XX
 FH Key Location/Qualifiers
 FT CDS 27..1214
 FT /tag= a
 FT /label= desaturase

XX
 PN W09113972-A.
 XX
 PD 19-SEP-1991.
 XX

XX
 PE 14-MAR-1991; 91WO-U001746.
 XX
 PR 14-NOV-1990; 90US-0615784.
 PR 16-MAR-1990; 90US-0494106.
 PR 13-AUG-1990; 90US-0567373.
 XX

PA (CALG-) CALGENE INC.

PI Thompson G, Knauf V;

XX
 DR WPI: 1991-295627/40.
 DR P-PSDB; AAR14189.

XX
 PT DNA encoding a plant desaturase - used for modifying the said.
 PT fatty acid compsn. of plant cells and plant seeds

XX
 PS Disclosure; Fig 2; 128pp; English.

XX
 CC A desaturase was purified from C. tinctorius and sequenced. Based
 CC on this sequence, oligonucleotide probes were synthesised and used to
 CC screen a C. tinctorius embryonic cDNA library to obtain DNA (AA013963)
 CC encoding the desaturase. The DNA for the C. tinctorius desaturase was
 CC also used as a probe to isolate DNA encoding desaturase from Ricinus
 CC communis (AA013964), Brassica campestris (AA013965) and Simmondsia
 CC chinensis (AA013966).
 CC See also AA013963-69.

XX
 SO Sequence 1668 BP; 464 A; 325 C; 386 G; 493 T; 0 other;

Query Match 42.38; Score 568.8; DB 12; Length 1668;
 Best Local Similarity 68.98; Pred. No. 8.4e-150;
 Matches 821; Conservative 0; Mismatches 343; Indels 27; Gaps 2;

```

QY 111 ACCAGTACCAGAGTTAGCTTCCAGGGTTTTCATGGCTCCAGTCTCAACTACTC 170
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 89 ACCAATGGCCAGACCAATCTCTAAGTTCTACATGGCTTCAAGTCTGGTTC 148
QY 171 CATGTTCTGATTAATCTCAAAAGTCC-----GCCAATCTTCAAGT 212
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 149 TAGAGAAAGTTGAATGTCAAGAAAGCTTTCATGCTCCCTGGGAGGTACATGTCAGT 208
QY 213 CACTACTCTATGCCACCCCAAAAGCTAGAAATATTCAGTCCCTTGATGATGGCTAG 272
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 209 TACCCATCTATGCCACCCCAAAAGATGATCTTAAATCCCTAGACAAATGGGCTGA 268
QY 273 GAACATGTGTGATTCACCTCAATCTGCGGAAATCTTGGCAACCCAAACACTACTT 332
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 269 GGAGAACATCTGGTTCATCTGTAAGCCAGTGGAAATGTGGCAACCCGAGATTTTTC 328
QY 333 GCCGATCCGCGTGTACAGAGGATTCAGAGCAAGTCGGGAGTTGAGGAAAGGCCAA 392
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 329 GCCAGATCCCGCTCTGATGATTTGATGAGCAAGTCAGGAACTCAGGAGAGAGCAAA 388
QY 393 GGAGATTCGCGAGCACTATTTGTGTGTTAGTTGAGATATGATCAGAGAAAGCACT 452
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 389 GGAGATTCGATGATTAATTTGTGTTGTTGAGAGACATGATTAACGGAAGAGCCCT 448
QY 453 TCCACATATATGTCTATGCTCAATAGTGTGATGATTAAGATGAGACTGGGCTGA 512
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 449 TCCCACTTCTCAAAACAATCTGATGATCTTGATGAGTGGGATGGAACAGTGCAG 508
QY 513 GCCCAGTCTGTGGCAATGTGAGCTAGGGCATGAGACTGCCGAGAGAAATAGACATG 572
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 509 TCCCTACTTCTTGGGCAATTTGGACAAGGGCATGAGACTGCCGAGAGAAATAGACATG 568
QY 573 CCTTCTCAATTAAGTACTTATTTTGTGTGAAAGGTTGATATGAGGAAATGAGAGAC 532
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 569 CTTCTCAATTAAGTACTTATCTTACTATCTGAGACAGTGAACATGAGCAAAATGAGAGAC 528
QY 633 TATTCATATCTCATGGGCTCAGAGATGGATATCAAGTCAAGAAACGCCCTACCTAGG 592
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 629 AATTCATATTTGATGTTGTTGATGATGATGATGATGATGATGATGATGATGATGATG 588
QY 693 CTTCATCTACATCTCTCTCCAGAGAGACACCTTCATATCCATGCCAACAGACCAA 752
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 689 GTTCATCTATACATCTCTCTCCAGAGAGAGACACCTTCATATCCATGCCAACAGACCAA 748
QY 753 GCTGGCCCAACACTACGGCGACAAGAACTCGCTCACATCTGGCGCTCATCGCTCCGA 312
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 749 ACAAGCCAAAGACATGAGACATAAAGTTGGCTCAAAATGTGTGATGATGATGATGATG 308
QY 813 CGAAGAGCCGCAAGCCACACACCTACACCAAGATCGTGGAAAAGCTGCTAGATCCACC 372
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 809 TGAGAAAGCCGCAATGAGACACGCTTACACAAAGATAGTGGAAAAGCTTTGAGATTGATCC 368
QY 873 CGACACACAGATTAATGCTTTTTCAGATATGATGCCCAAAAATAACATATGCGACGCA 932
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 869 TGATGAACTGTTTGGCTTTTCTGATATGATGAGAAAATAATTTCTATGCTGTGACA 928
QY 933 CTTCATGTAACGAGAGTACACTCTTTTAAACATTTGACGCGGTGTCTCTAGAG 992
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 929 CTTCATGTAATGATGAGAGATGATATCTTTTGAACACTTTTTCAGCTGTGGCAGCG 988
QY 993 AGTNGGGTTTATTCGCGTGTGATATTCGACATCTTGAAGTTCCTGCTGATTAATG 1052
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 989 TCTTGGAGTCTACACAGCAAAAGATTAATGATTAATGAGATCTTCTGTGGCAATG 1048
QY 1053 GAATGTGAAGAGCTTACGGGCTGTGCGAGAGGGCGGAAGACCGCAAAATATGTTG 1112
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1049 GAAGGTGGAATAACTAACGGGCTTTCAGCTGAGGACAAAGGCTCAGACATATGTTTG 1108
QY 1113 TGAATTTGGTCCCAAGATTAAGCGAGTGAAGAGAAAGTCCAGGGGAGAGAGAAAGAA 1172
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1109 TCGGTTTACCTCCAAAGATTAAGAGGCTGCAGAGAGAGCTCAAGAGAAAGGCAAG----- 1163
QY 1173 GAAAGTGAAGACACCTGTTTCTTCAGCTGATTTTCAATCGGAGTTGAAGATATGAC 1232

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Db 1164 -----GAAGCACCCACCATGCTTTCAGCTGATGATGAGCAAGTAAAGTCTAGT 1219
QY 1233 AGGAAGGGAAGGAATGAGAGAGCAATGATGATGATGATGATGATGATGATGATG 1283
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1220 GGCTAAAGTGAAGAGCAAAACCAAAATGTTAGTTTCACTCTTTTCATGCG 1270

```

RESULT 5
AAC84531
ID AAC84531 standard; DNA: 1092 BP.
XX
XX AAC84531;

XX 02-APR-2001 (first entry)
XX Mature castor enzyme encoding DNA.
DE

XX Castor; delta9-18:0-acyl carrier protein desaturase; ACP; enzyme;
KW vegetable oil; fatty acid; nutrition; plant oil; mutant; ds.
OS Ricinus communis.
XX

FH Key Location/Qualifiers
FT CDS 1..1092
FT /tag= a
FT /product= "mature castor enzyme"
XX
XX WC200075170-A1.
XX
XX 14-DEC-2000.
XX
XX 08-JUN-2000; 2000MO-US15741.
XX
XX 09-JUN-1999; 99US-0328550.
XX

PA (BROO-) BROOKHAVEN SCI ASSOC LLC.
XX
XX Shanklin J;
XX
XX WPI: 2001-091202/10.
XX
XX P-PSDB: AABA8199.
XX

PT New mutant castor Delta9-18:0-Acyl Carrier Protein desaturase, useful
in producing commercially valuable products, e.g. vegetable oils useful
in human nutrition or as industrial chemicals
XX

PS Example; Fig 1; 53pp; English.

XX The invention relates to a new mutant castor Delta9-18:0-acyl carrier
XX protein (ACP) desaturase that has one or more amino acid substitutions
XX selected from: (a) Ala for Met at residue 114; (b) Arg for Thr at residue
XX 117; (c) Gly for Leu at residue 118; (d) Val for Pro at residue 179; (e)
XX Val for Thr at residue 181; (f) Leu for Gly at residue 188; and (g) Phe
XX for Thr at residue 181. The mutant castor Delta9-18:0-ACP desaturase is
XX useful in producing commercially useful products, such as Vegetable oils
XX rich in monounsaturated fatty acids. Such vegetable oils are important in
XX human nutrition and can be used as renewable sources of industrial
XX chemicals. A method for specifically altering a function of a protein
XX through directed mutagenesis is also provided. The method can be used
XX altering enzymatic functions, binding functions or structural functions
XX of the castor desaturase enzyme. The method is also useful for
XX manipulating the physical properties and commercial uses of conventional
XX plant oils. The present sequence represents the DNA encoding a mature
XX castor enzyme.

SQ Sequence 1092 BP; 318 A; 214 C; 282 G; 278 T; 0 other;

Query Match 41.4%; Score 555.8; DB 22; Length 1092;
Best Local Similarity 72.1%; Pred. No. 3.1e-146;
Matches 741; Conservative 0; Mismatches 278; Indels 9; Gaps 1;

QY 201 AATCTTCAAGTCACTCACTATGCAACCCCAAAAGCTAGAAATATTTCAAGTCCCTTGA 260

```
Db 72 ACATGTTACAGTTACCATTTCTATGCCCACCCCAAAAGATTGAGATCTTTAAATCCCTAGA 131
Qy 261 TGAATGGGCTAGAGAACAAATGTGTGATTCACCTCAATCTGTGAGAAATCTTGGCACCC 320
Db 132 CAATTTGGGCTGAGAGAGAAATCTGTTCATTCGAAAGCCAGTTGAAATGTTGGCAACC 191
Qy 321 ACAAGACTACTTCCCGATCCGGTGTGACAGGATTCGAGAGCAATGCGGAGTTGAG 380
Db 192 GCGAGATTTTTTCCAGATCCCGCTCTGTGATTTGATGAGACAACTCAGGGACTCAG 251
Qy 381 GGAAGAGGCCAAGAGATTCGCCAGACATATTTTGTGCTTATAGTTGAGATGATCAC 440
Db 252 GGAGAGAGCAAAAGAGATTCCTGATGATTTTGTGTTGTTGGTGGAGACATGATTAAC 311
Qy 441 AGAAGAAAGCACTTCCAAATATATGCTATGCTCAATAGTGTGATTTAAGATGA 500
Db 312 GGAAGAAAGCCCTTCCCACTTATCAACAAATGCTGAATACCTTGGATGGAGTTCCGGATGA 371
Qy 501 GACTGGGGCTGAGCCAGTGTGAGCAATGTGAGCAATGAGCTGCGAAGAGAA 560
Db 372 AACAGGTGCAAGTCCGACGCTTGGGCAATTTGGACAAAGGCACTGCGGAGAGAA 431
Qy 561 TAGACATGCTGACCTTCTCAATAAGTACCTTTATTTGCTGGAAGGGTTGATATGAGAA 620
Db 432 TAGACATGCTGACCTCTCAATAAGTATCTCTACCTATCTGAGAGATGAGACATGAGCA 491
Qy 621 AATTGGAAGCAATTTCAATATCTCAATCGGCTGAGCAATGATATCAAGTCAGAAACAG 680
Db 492 AATTGGAAGCAATTTCAATATGATGATGCTGAGCAATGATGCTGCGGAGCAAAACAG 551
Qy 681 CCCCTACCTAGGCTCATCTACACATCCCTTCAAGAGAGAGCAACCTTCATATCCCATGC 740
Db 552 TCCATACCTTGGGTTGATCATATCATCATCTCCAGAAAGGCAACCTTCATTTCTCATGG 611
Qy 741 CAACACAGCCAGCTGCGCCCAACACTAGCGGACAGCAAGAACCTGCTGCATCTCGGCTC 800
Db 612 GAACACTGCGCCGACAAAGCCAAAGAGCATGAGACATTAAGTTGGCTCAAAATATGCTGAC 671
Qy 801 CATTGCTCCGAGAGAGAGGCGCACGACCTACACCAAGTCTGGAAGAAAGCTCGC 860
Db 672 AATTGCTGAGATGAGAGAGCGCATGAGACGCTTACACAAAGATAGTGAAGAAACCTTT 731
Qy 861 TGAATGACCCCGACACAAACAGTAATGCTTTCAGATATGATGAGCAAAAAAATAAC 920
Db 732 TGAATGATGATTCGATGATGATACCGTTTGGCTTTTCCGATATGATGAGAAAGAAATTC 791
Qy 921 AATGCAAGCGCACTTGAATGATGAGAGAGAGTACGAACTTCTTTTAACATTTTCACGGC 980
Db 792 TATGCTGACACTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 851
Qy 981 GGTGCTCAGAGAGTNGGTTTATCTGCTGTTGATATTTGAGCACTTTAGAGTTCT 1040
Db 852 TGTGTCGACAGCGCTTGTGATCTTACACAGCAAAAGATTAATGATTAATTTGGAGCTCT 911
Qy 1041 GGTGATTAATGATGATGAGAAAGCTTACGGGCTGTGAGAGAGAGGCGGCAAAAGCGCA 1100
Db 912 GGTGGGCAAGTGAAGTGAATTAAGTAAAGGCGCTTTCAGCTGAGGAGCAAAAAGGCTCA 971
Qy 1101 GGAATATGTGTGTAATTTGGGTCCTCAAGATTTAGGCGAGTGAAGAGAAAGTGCAGGGAA 1160
Db 972 GGAATATGTGTGTAATTTGGGTCCTCAAGATTTAGAAAGGCTGGAAGAGAGAGCTCAAGGAG 1031
Qy 1161 GGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1220
Db 1032 GGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1082
Qy 1221 GAAGATAT 1228
Db 1083 GAAGCTGT 1090
```

RESULT 6

```
AA013963
ID AA013963 standard; DNA; 1533 BP.
XX
AC AA013963;
XX
DT 11-DEC-1991 (first entry)
XX
DE C. tinctorius delta9 desaturase from pCGN274.
XX
KW Desaturase; probe; ss.
XX
OS Carthamus tinctorius.
XX
FH Key location/Qualifiers
FT CDS 106..1294
FT mat_peptide 106..204
FT /tag= a
FT /label= desaturase
FT /tag= b
FT /tag= c
XX
PE WO9113972-A.
XX
PD 19-SEP-1991.
XX
PF 14-MAR-1991; 91MO-U001746.
XX
PR 14-NOV-1990; 90US-0615784.
PR 16-MAR-1990; 90US-0494106.
PR 13-AUG-1990; 90US-0567373.
XX
PA (CALG-) CALGENE INC.
XX
PI Thompson G, Knauf V;
XX
DR WPI: 1991-295627/40.
DR P-PDB; AAR14188.
XX
PT DNA encoding a plant desaturase - used for modifying the satd.
PT fatty acid compsn. of plant cells and plant seeds
XX
PS Disclosure: Fig 2; 128bp; English.
XX
CC The cDNA comprises a poly(A) track at the 3' end of 100-200 bases.
CC A desaturase was purified from C. tinctorius and sequenced. Based
CC on this sequence, oligonucleotide probes were synthesised and used to
CC screen a C. tinctorius embryo cDNA library to obtain DNA encoding the
CC desaturase. The DNA for the C. tinctorius desaturase was also used as
CC a probe to isolate DNA encoding desaturase from Ricinus communis
CC (AA013964), Brassica campestris (AA013965) and Simmondsia chinensis
CC (AA013966).
CC See also AA013963-69.
XX
SQ Sequence 1533 BP; 420 A; 327 C; 392 G; 394 T; 0 other;
XX
Query Match 38.8%; Score 522; DB 12; Length 1533;
Best Local Similarity 68.5%; Pred. No. 1.3e-136;
Matches 739; Conservative 0; Mismatches 331; Indels 9; Gaps 1;
```

```
Db 421 TCTGAAGGATTTGATGAACAAGTCAAGAACTAAGGCAAGACAAAGGATTTCTGAT 480
Oy 406 GACTATTTTGTGGTGTAGTGGAGATATGATCAGAGAAACACTTCCACATATATG 465
Db 481 GATTACTTTTGTGTTTGTGGAGATATGATATACAGAGAACCCCTACTACTTACCAA 540
Oy 466 TCTATGCTCAATAGTGTATGTATTAAGGATGAGACTGGGGCTGAGCCACTGCTTGG 525
Db 541 ACAATGCTTAATGACCTAGATGCTGATGATGAGATGAGACTGGGGCTGAGCCCTTGG 500
Oy 526 GCAATGTGACTAGGACTGAGCTGCCGAAGAAATAGACATGATGACCTTCCATTAAG 585
Db 601 GCTGTGTGACTAGGCTTGGACAGCTGAAGAGAACAGCATGGCATCTTCCACACC 660
Oy 586 TACCTTATTTGTCTGGAAGGTTGATATGAGAAATTGAGAGACTATTCATATCTC 645
Db 661 TATCTCTACTCTTCTGGGGGGGTAGACATGAGACATACAGAAACATTCAGTATCTC 720
Oy 646 ATCGGCTCAGAAATGATATCAAGTCAAGAAACAGCCCTTACCTAGGCTTCATCTACAC 705
Db 721 ATTTGGGTCAAGATGATGATCTGCTACCGAAACAGCCCTTACCTTGGCTCATCTACACA 780
Oy 706 TCCCTCCAGAGAGACCACTTCATATCCCATGCCAACACAGCCCAAGCTGGCCCAACAC 765
Db 781 TCGTTTCAAGAGCGTCCCACTTTGTTCTCAGAGAAACACCGCCAGGCTGCAAGAGAT 840
Oy 766 TACGGGACAGAACCTCCCTCCTCATCTCGGCTCCATCGCCCTCCACAGAGAGCCGAC 825
Db 841 CATGGGAGAGTGAATGCGCGCAATTTGTGTACATCCGCTGTGACGAAAGCCGCTCAC 900
Oy 826 GCCACAGCCTTACACCAAGATCTGTGAAGAAAGCTCGTGAGATCGACCCGACACACAGTA 885
Db 901 GAGACCGCTTATACCAAGATAGTCGAAAGCTATTCGAGATCGATCTGTGACCGCTT 960
Oy 886 ATTTGCTTGCAGATATGATGCGCAAAATAATACAAATGCCACGCACTTGATGTACGAC 945
Db 961 CTGTGCTTTGCGCAGATGATGAGAAAGATTCGATGCCGCGCACCTGATGTACGAT 1020
Oy 946 GGAAGTGAAGAACTTTTAAACATTTTCACGCGGTTGCTGAGAGATGNGGCTTAT 1005
Db 1021 GGGCGGTGATGACAACTCTTTCGAACTTTCTGCGGGTTGCCAAAGACCTGGCGCTTAC 1080
Oy 1006 TCTGCGTGTGATTTATTCGACATCTTAAAGATTTCTGTGTGATTAATGAAATGTGAAAG 1065
Db 1081 ACCGCGCAAGACACTACCGCACATCTGGAATTTCTGTGCGGCGGAGGAGCGGAT 1140
Oy 1066 CTTAGCGGGCTGTGCGAGCAGAGGGGGAAGAAAGCGCAGGAATATGTGTGATTTGGTCCC 1125
Db 1141 TTGACCGGCGCTATCTGTGAAGGGCGTAAAGCGCAAGATTATGTGTGGGTTGCCACCA 1200
Oy 1126 AAGATTAGCGAGTGAAGAGAAAGTGCAGGGGAGAGAGAGAAAGAAAGCTTGAGCAC 1185
Db 1201 AGAATCAGAAAGCGTGAAGAGAGAGCTCAAGGCGAGCAAG-----GAAAGGACT 1251
Oy 1186 CCTGTTTCTTCACTGATTTTCAATCGGAGTTCAACATATGAACAGAGAGGAGG 1244
Db 1252 GTTGTTCATTCAGCTGATTTTTCGATAGACAGGTGAAGCTGTGAAGAAAGAAAAAAGCG 1310
```

RESULT 7
AAQ22616
ID AAQ22616 standard; DNA; 1533 BP.
XX

XX AAQ22616;
XX 07-JUL-1992 (first entry)
XX

DE Carthamus tinctorius desaturase gene.
XX

XX Safflower; fatty acid synthesis; seed; acyl carrier protein;
KM lipids; ss.
XX

```
OS Carthamus tinctorius.  
XX  
XX Key Location/Qualifiers  
XX CDS 105..1294  
XX FT /*tag= a  
XX FT /product= desaturase  
XX  
XX MO9203564-A.  
XX  
XX PD 05-MAR-1992.  
XX  
XX PE 15-AUG-1991; 91MO-U005801.  
XX  
XX PR 26-JUN-1991; 91US-0721761.  
XX PR 15-AUG-1990; 90US-0568493.  
XX  
XX PA (CALG-) CALGENE INC.  
XX  
XX PI Knaut VC, Thompson GA;  
XX  
XX DR WPI: 1992-096907/12.  
XX DR P-PDB: AAR22048.  
XX  
XX PT New plant beta-keto:acyl synthase protein - obtd. from Ricinus  
XX PT communis, useful e.g. for modifying fatty acid compns.  
XX  
XX PS Disclosure: Fig 8: 157pp; English.  
XX  
XX CC The desaturase gene isolated from Carthamus tinctorius was present  
XX CC as the clone pGKN254. The clone can be used to construct: acyl  
XX CC carrier protein expression cassettes in a binary vector for plant  
XX CC transformation. This allows integration of nucleic acids encoding  
XX CC a desaturase sequence and a synthase sequence into the genome of a  
XX CC host cell. A plant desaturase includes any enzyme capable of  
XX CC catalysing the insertion of a first double bond into a fatty acid  
XX CC -ACP moiety especially between C9 and C10.  
XX CC See also AAQ22606-21.  
XX  
XX SQ Sequence 1533 BP; 421 A; 327 C; 391 G; 394 T; 0 other;  
XX  
XX Query Match 38.8%; Score 522; DB 13; Length 1533;  
XX Best Local Similarity 68.5%; Pred. No. 1.3e-136;  
XX Matches 739; Conservative 0; Mismatches 331; Indels 9; Gaps 1;
```

```
Db 661 TATCTTACCTTTTGGGGGGGTAGACATGAGGCGATACAGAAACAAATTCAGTATCTC 720
QY 646 ATCGGCTCAGGAATGATATATCAAGTCAGAAAACAGCCCTACTATGAGCTTATCTACACA 705
Db 721 ATTGGGTCAGGAATGATATCTCTGACCGAATAAAGCCCTTACCTTGGTTATCTACACA 780
QY 706 TCCCTTCCAGAGAGACACCTTCAATATCCATGCCAACACAGCCCAAGCCCAACAC 765
Db 781 TCGTTTCAAGAGCGCTGCACATTTGTTTCTCACGAAAACACCGAGCATGCAAAAGAT 840
QY 766 TACGGCGCAAGAACCTCGCTCACATCTGGGGCTCCACATCGGCTCCGAGAGAACGGCCAC 825
Db 841 CATGGGACGTGAACTGGCCCAATTTGTGTACAAATCGGCTGTGAGAAACCGCTCAC 900
QY 826 GCCACAGCTACACCAAGATCGTGGAAAAGCTCGCTGATGCAAGCCCGACACACACATA 885
Db 901 GAGACCGCTTATACAAAGATATGCGAAAAGCTATTCGAGATCGATCTGATGGCACCGTT 960
QY 886 ATTGCTTTTGCAGATATGATGCGCAAAAAATAACAATGCCAGCCACTTGATGTAGCAC 945
Db 961 CTTCCTTTTGGCCAGATGATGAGAAAAGATCTCGATGCCCGCACACTTGATGTAGCAT 1020
QY 946 GGAAGTACGCAACTCTTTTAAACATTTCAGCGCGGTGCTGACAGAGTNGCCTTAT 1005
Db 1021 GGGCGTATATCAACCTCTTGAACATTTCTCGGGGTGGCCAAAGACTCGGCTCAC 1080
QY 1006 TCTGCGTTGATTAATTCGACATCTTATAGATTTCTGTGATTAATTAATGAAAG 1065
Db 1081 ACCGCCAAAGACTACGCGCATCTGGAATTTCTGCGCGCGTGGAAAGTGGCGGAT 1140
QY 1066 CTACAGGGGCTGTGCGACGAGGGCCAAAGCCGACGAAATATGTGTGAATTTGGTCCC 1125
Db 1141 TTGACCGGCTATCTGTGTGAAGGCGCTTAAAGCGCAAGATTATGTTTGGGTTCCACA 1200
QY 1126 AAGATTAGCGAGTGAAGAGAAAGTGCAGGGAGGAGAGAAAGAGAAAGCTGACAC 1185
Db 1201 AGATATCAGAGGCTGAGGAGAGAGCTCAAGGGCGAGCAAG-----GAAGGACT 1251
QY 1186 CCTGCTTTCTTTCACTGAGATTTTCAATCGGAGTTGAAGATATGACAGAGAGGAGG 1244
Db 1252 GTTGTTTCATTCAGCTGATTTTCGATATGACAGGTGAAGCTGTGAACAAAAAAGCG 1310

RESULT 8
ID AA064003 standard; cDNA; 1533 BP.
AC AA064003;
XX
DT 01-DEC-1994 (first entry)
XX
DE Sequence encoding desaturase enzyme.
XX
KW Synthase; plants; oil; seed; fatty acids; gene expression;
XX biosynthesis; ss.
OS C. tinctorius.
XX
FH Key Location/Qualifiers
FT CDS 106..1296
FT /tag= a
FT /product= Desaturase.
FT sig_peptide 106..211
FT /tag= b
FT mat_peptide 212..1296
FT /tag= c
XX
PN WO9410189-A.
XX
PD 11-MAY-1994.
XX
PF 02-NOV-1993; 93WO-US10526.
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XX
PR 02-NOV-1992; 92US-0971182.
XX
XX (CALJ ) CALGENE INC.
PA
XX
PI Knaufl VC, Thompson GA;
XX
DR WPI: 1994-167378/20.
XX
XX P-PSDB: AAR54033.
XX
PT DNA constructs encoding beta-(keto:acyl)-ACP synthase - useful to
PT modify the oil content of seeds, e.g. for dietary purposes
XX
XX Disclosure; Figure 10; 85pp; English.
XX
XX
XX Higher plants appear to share a common metabolic pathway for the
CC synthesis of fatty acids. Genes encoding synthase proteins may be
CC used in nucleic acid constructs to modulate the amount of synthase
CC activity in a host cell. Nucleic acid constructs may also be
CC designed to decrease the expression of a synthase protein, i.e.,
CC constructs containing anti-sense synthase sequences. The constructs
CC allow the generation of plants bearing seeds which have enhanced oil
CC yields and/or altered compositions of oils. The production of
CC common plant unsaturated fatty acids is catalysed by a desaturase.
CC Oleic, linoleic and alpha-linoleic acids found in storage
CC triglycerides are produced from the desaturation of stearoyl-ACP to
CC form Oleoyl-ACP.
XX
SQ Sequence 1533 BP; 420 A; 327 C; 392 G; 394 T; 0 other;
```

Query Match 38.8%; Score 522; DB 15; Length 1533;
Best Local Similarity 68.5%; Pred. No. 1,3e-136;
Matches 739; Conservative 0; Mismatches 331; Indels 9; Gaps 1;

```
QY 166 AACTCCATGGTTCTTGTAATTCGAAAAGTCCGCCAATCTTCAAGTCACTCACTATG 225
Db 241 AATGCCAAGAAAGCTTTTCAACCTCCACGAGAGGTTCTATGAGGACGACCTCCATG 300
QY 226 CCACCCCAAGAGCTAGAAATATTCAGTCCCTGATGATGGGCTGGACATATGTTG 285
Db 301 CCACACAGAGATAGAGATTTTCAATTCATGAGGCTTGGCTGAGCAACATATTTG 360
QY 286 ATTACCTCAAAATCTGTGAGAAATCTTGGCAACACAGACTACTTCCGGATCCGGTG 345
Db 361 GTTCACCTAAGCCAGTGGAGAAATGTTGGCAAGCAGAGATTTCTTCCGGACCTCGCA 420
QY 346 TCAAGAGGATTCAGAGAGCAAGTCCGGAGTTAGGAGAAAGGCCAAGAGATTCGGAC 405
Db 421 TCTGAAGGATTTGATGAACAAGTCAAGGAACTAAGGCAAGAGCAAGAGATTCCTGAT 480
QY 406 GACTATTTTGTGTGTTAGTTGAGATATGATCAGAGAAAGCAACCTCCACATATATG 465
Db 481 GATTACTTTCTTTTGGTGGATATGATATACAGAGAAACCTTACTCTTACCAA 540
QY 466 TCTATCTCAATAGTGTGATGATTAAGATGAGACTGGGCTGAGCCCAAGTCCGTGG 525
Db 541 ACAATGCTTAATACCTAGATGTTGATCGATGAGAGACTGGGCTGACCTTACGCTTGG 600
QY 526 GCAATGTGACTAGGCGATGACTGCCGAAGAGATATGATGTGATCTTCAATTAAG 585
Db 601 GCTGTCTGAGATGAGGCTTGAGCAGCTGAAGAAACAGGCAATGCGCATCTCCACACC 660
QY 586 TACCTTATTTTGTCTGAGAGGGTTGATATGAGGAAATGAGAGACATTCATATATCTC 645
Db 661 TATCTTACCTTTTCTGGGGGTAGACATGAGGCAATACAGAGCAATTCAGTATCTC 720
QY 646 ATCGGCTCAGGAATGATATCAAGTCAAGAAACAGCCCTTACTAGAGCTTCTTACACA 705
Db 721 ATTGCGTCAAGATGATATCTCTGACCGAATAAAGCCCTTACCTTGGTTATCTACACA 780
QY 706 TCCCTTCCAGAGAGACACCTTCAATATCCATGCCAACACAGCCCAAGCCCAACAC 765
Db 781 TCGTTTCAAGAGCGCTGCACATTTGTTTCTCACGAAAACACCGAGCATGCAAAAGAT 840
```

Oy	766	TACGGGACAAGAAACCGCTCACCATCTCGGTGCCTCATCGCCCTCCGACGAGAAGGCCAC	825
Db	841	CATGGGACGTAACACTGGCGCAAAATTGTGGTACATCGCTCTGACGAAGAAGGCTAC	900
Oy	826	GCCACACCCCTACACCAAGATCGTGAAAAAGCTCGTAGAATCGACCCCGACACACAGTA	885
Db	901	GAGACGCCCTATATCAAAAGATAGTCGAAAAGCTATTGCAATGATGATCTGATGGCACGCTT	960
Oy	886	ATTGCTTTTGCAGATATGATGCCAAAAAATAATACATGCCACGCCACTTGATTAGAC	945
Db	961	CTTCTCTTTTCCCGACATGATGAGAAAAAAGATCTCATGCCGACACTTGATTGATGAT	1020
Oy	946	GGAAGTACGCAACTCTTTTTAAACATTACGGCGGTTGTCAGAGAGTGGGTTTAT	1005
Db	1021	GGGGGTATGACAAACCTCTTCGAAACATTTCTCGGGCGTTGCCCAAAGACTCGGCTTAC	1080
Oy	1006	TCTCGTTGGATTATTTCCGACATCTTAGAGTTTCTGTGGATTAATGGAATGTGGAAG	1065
Db	1081	ACCCCCAAAGACTACGCGCGACATCTGGAATTTCTGTGGCGGGTGAAGATGCGCAT	1140
Oy	1066	CTTACGGGGGCTGTGACGCGGGGGCGAAAAAGCCAGATATGTGTGAATTGGGTGCC	1125
Db	1141	TTTGACGGGCTATCTGGTGAAGGGCCGTAAGGCCAAGATTATGTTGGCGGTGGCACCA	1200
Oy	1126	AAGATTAGGGAGTGGAGAGAAAGTGCAGGGGAAAGAGAACAAAGAAAGAAAGCTGACAC	1185
Db	1201	AGATTACGAAGGCGTGGAGGAGAGAGCTCAAGGGCGAGCAAG-----GAAAGACT	1255
Oy	1186	CGTGTCTTTCACGTGTGATTTTTCATCGGGAGTTTAACATATGAACAGGAAGGACAG	1244
Db	1252	GTGTGTCCATTACCTGTGATTTTTCGTATGACACAGTCAACCTGTGAAGAAAAAAAAGC	1310

RESULT	9
AAV15250	
ID	AAV15250 standard; cDNA to mRNA; 1533 BP.
XX	
AC	AAV15250;
XX	
DT	28-MAY-1998 (first entry)
XX	
DE	Carthamus tinctorius desaturase from cDNA clone pCGN2754.
XX	
KW	Carthamus tinctorius; safflower; delta-9 desaturase; oilseed;
KW	fatty acid saturation; ds.
XX	
OS	Carthamus tinctorius.
XX	
Key	Location/Qualifiers
FH	106..1296
FT	CDS
FT	/*tag= a
FT	/product= "desaturase"
FT	106..204
FT	/*tag= b
FT	mat_peptide
FT	205..1293
FT	/*tag= c
XX	
PN	US5723595-A.
XX	
PD	03-MAR-1998.
XX	
PF	06-JUN-1995; 95US-0471791.
XX	
PR	16-SEP-1991; 91US-0762762.
PR	16-MAR-1990; 90US-0494106.
PR	13-AUG-1990; 90US-0567373.
PR	14-NOV-1990; 90US-0615784.
PR	14-MAR-1991; 91WO-US01146.
PR	06-JUN-1995; 95US-0471791.
XX	
PA	(CALJ) CALGENE INC.
XX	

PI	Knauf VC, Thompson GA;
XX	
DR	WPI: 1998-178544/16.
DR	P-PSDB: AAW44349.
XX	
PI	DNA encoding plant delta-9 desaturase protein - having amino acid
PT	sequence of <i>Carthamus tinctorius</i> desaturase, useful for, e.g.
PT	producing oil-seeds with modified levels of fatty acid saturation
XX	
PS	Example 5; Column 51-54; 87pp: English.
XX	
CC	The present sequence encodes a <i>Carthamus tinctorius</i> desaturase from
CC	clone pCG2754. The present invention describes a recombinant DNA
CC	construct comprising a DNA sequence encoding a plant Delta-9 desaturase
CC	protein. The present invention also provides a method of modifying fatty
CC	acid composition in a host plant cell from a given fatty acid saturation
CC	to a different fatty acid saturation, comprising growing a host plant
CC	cell containing a recombinant DNA sequence which encodes a plant
CC	desaturase under the control of regulatory elements functional in the
CC	plant cell during lipid accumulation. Also, oilseeds having a modified
XX	level of fatty acid saturation and oils produced from such oilseeds.
SO	Sequence 1533 BP; 420 A; 327 C; 392 G; 394 T; 0 other;

	Query Match	38.8%	Score 522	DB 19	Length 1533	
	Best Local Similarity	68.5%	Pred. No. 1.3e-116			
	Matches 739	Conservative 0	Mismatches 331	Indels 9	Gaps 1	
QY	166	AACCTCAGTGGTTCCTGATATCTCAAAAGTCGCGCAATCTCTCAAGTCACATCCTATG	225			
DB	241	AATGCCAAGAGCCCTTTTCAACCTCCAGAGAGGTTCATGTTTCAGGTACGACATCCATG	300			
QY	226	CCACCCCAAAGCTTGAAATATTTCAAGTCCCTTGATGATTGGGCTAGACAAATGTGTTG	285			
DB	301	CCACACAGAGAGATGAGATTTTCAAAATCCATCGAGGGGTGGGCTGACACAGCATATATG	360			
QY	286	ATTCACTCAAAATCTGTGAGAAATCTTGCGAACCAACAAAGCTACTTTCGGATCCGGTGG	345			
DB	361	GTTCACCTTAAGCCAGTGGAGAAATGTTGGCAGACAGGATTTCTTCCGAGCCTTCA	420			
QY	346	TCAGACGAGATTCGAGACCAAGTCGCGGAGATTTGAGAGAAAGGCCAAGAGATTCGCCAC	405			
DB	421	TCTGAAGGATTTGATGAAACAGTCAAGGACACTAAGGCAAGGCAAGCAAGAGATTCCTGAT	480			
QY	406	GACTATTTTGTGGTGTAGTTAGTATGATCAGACGAAGACACTTCCAAATATATG	465			
DB	481	GATTACTTTGTTGTTGGTTGGATGATGATTACAGAGAAAGCCCTACCTACTTACCA	540			
QY	466	TCTATGCTCAATAGTGTGATGTTTAAGATGAGATCGGGGCTGAGCCAGTCTGG	525			
DB	541	ACAAATGTTAAATACCTAGATGCTAGCTGTAGACTGGAGCTGGGCTTAGGCTTACGGCTGG	600			
QY	526	GCAATGTGAGACTAGGGACATGAGCTCCGAGAGATAGCATGATGGACCTTCTCAATAG	585			
DB	601	GCTGTCTGACTAGGGCTTTGACAGCTGAGGAACAGGACGATGGGATCTTCTCACACC	660			
QY	586	TACCTTATTTTGTCTGGAAGGGTGTATATGAGGAATTTGAGAAACATCTATCAATATTC	645			
DB	661	TATCTCTACCTTTCTGGGGGGGTAGACATGAGGACGATACAGAAACAAATTCAGTATCTC	720			
QY	646	ATCGGCTCAGGANTGATATCAATGTCAGAAAAACAGCCCTTACCTAGCTTCATCTACACA	705			
DB	721	ATTGGGTGAGGANTGATCTCTGATCCGAAAAACGCCCTTACCTTGGGTTCACTATACACA	780			
QY	706	TCTCTTCAAGAGAGACAACTTCATATTCATGCGCAACACAGCCCAAGCTGTGCCAACAC	765			
DB	781	TCTGTTTCAAGACCGTGCACATTTGTTTCTCAGGAAACACCGCCAGGCTATGCAAAAGAT	840			
QY	766	TACGGCGCAAGACCTCGCTCACATCTGCGGCTCCATCTCGGAGAGAAAGGCCAC	825			
DB	841	CATGGGAGCGTAACACTGGCCCAATTTGTGTACAAATCGCGTCTGACGAAAAAGGCTAC	900			
QY	826	GCCACAGCCTACCCCAAGATGCTGAAAAAGCTCGCTGAGATGACCCCGACACAAACAGTA	885			


```
RESULT 12
AA063437
ID AA063437 standard; cDNA; 1529 BP.
XX
XX AA063437;
AC
XX
XX 03-JUL-1997 (first entry)
DT
XX
XX
DE Rapeseed stearyl-ACP desaturase cDNA clone BND11.
XX
XX steroyl-ACP desaturase; rapeseed; acyl-ACP thioesterase;
KM stearic acid; transgenic plant; oilseed;
XX vegetable oil; mangosteen; Garcinia mangifera; ss.
OS Brassica napus cv. 212/86.
XX
XX
FH Key Location/Qualifiers
ET CDS 25..1230
ET /tag= a
XX
XX MO0912047-A1.
XX
XX 03-APR-1997.
XX
XX
XX 30-SEP-1996; 96WO-US16078.
XX
XX
XX 29-SEP-1995; 95US-0537083.
XX
XX (CALJ ) CALGENE INC.
XX
XX Knauf VC, Kridl J, Lassner MW;
XX
XX WPI; 1997-212906/19.
XX
XX P-PSDB; AAM14797.
XX
XX
XX Increasing levels of stearate in plant seed triglyceride(s)
PT using a DNA sequence encoding acyl-ACP thioesterase protein having
PT substantial activity on C18:0 acyl-ACP substrates
XX
XX
XX Example 5; F196A-6C; 55pp; English.
XX
XX A cDNA clone (AA063437), designated BND11, codes for oilseed rape
CC stearyl-ACP desaturase (AAM14797), an enzyme that catalyses the
CC desaturation of stearyl-ACP (C18:0) to oleoyl-ACP (C18:1). BND11
CC and clone BND9 (see also AA063438) were isolated from a cDNA library
CC constructed from RNA obtd. from mid maturation seeds of Brassica
CC napus cv. 212/86. The library was screened with the coding region
CC of a delta-9 desaturase gene from Brassica campestris. An antisense
CC gene was constructed to generate antisense RNA homologous to both
CC BND9 and BND11. In transgenic Brassica plants expressing the
CC stearyl-ACP desaturase antisense construct and mangosteen Class I
CC acyl-ACP thioesterase Garmfalai (see also AAM14795), levels of C18:0
CC in the seed oil may exceed 50% of total fatty acids.
XX
XX
XX Sequence 1529 BP; 414 A; 351 C; 363 G; 401 T; 0 other;
SO
Query Match 38.8%; Score 521.4; DB 18; Length 1529;
Best Local Similarity 71.3%; Pred. No. 1.9e-136;
Matches 687; Conservative 0; Mismatches 277; Indels 0; Gaps 0;
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QY 386 GGGCCAAAGAGATTCCCGACGACTATTGTGGTGTAGTTGGAGATATCATCAGAG 445
DB 395 GAGCAAGAGAGACTCCCGATGATTAATCTCGTGTCTGGTGAGCATGATCAGAGAG 454
QY 446 AAGCACTTCCAAATATATGCTATGCTCAATGAGTGTGATTAAGATGAGAGCTG 505
DB 455 AAGGCTTCCACCTTCAAAACATGCTGAACACTTGGATGGTGAAGATGAGAGACTG 514
QY 506 GGGCTGAGCCAGTGTCTGGGCAATGTGAGCTAGGCGATGAGCTGCCAGAGAGATGAG 565
DB 515 GTGCTAGCCCCACTTCAATGAGCGCGTTTGACTGAGAGCTTGAGCTGCTGAGAGATGCC 574
QY 566 ATGCTGACCTTTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 625
DB 575 ACGGTGATCTTTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 634
QY 626 AGAAGACTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 665
DB 635 AGAAGACTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 694
QY 686 ACCTAGCTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 745
DB 695 ACCTTGGCTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 754
QY 746 CAGCCAAAGCTGGCCCAACACTACGCGGACAAAGCAACTCGCTCAATCTGCGGCTCCATCG 805
DB 755 CAGCTGGCCCAAGCCAAAGACGAGAGACTCAAGCTAAGCCCAATCTGCGGACATAG 814
QY 806 CCTCCGACGGAAGCGCCACAGCCCTACACCAAGATCGTGGAGAAAGCTGCTGAGA 865
DB 815 CTGCAAGCAGAAAGCGCTACAGAGAGCGCTTACACCAAGATGATTAAGATTAAGCTTCTGAGA 874
QY 866 TCGACCCCGACACAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 925
DB 875 TTGATCTGACGCGACTGTGTGCTGCTTTCGCGATTAATTAATTAATTAATTAATTAATTAAT 934
QY 926 CAGCGCACTTGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 985
DB 935 CTGCTCACTGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 994
QY 986 CTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1045
DB 995 CTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1054
QY 1046 ATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1105
DB 1055 GAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1114
QY 1106 ATGCTGTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1165
DB 1115 ATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1174
QY 1166 AGAA 1169
DB 1175 AGAA 1178
RESULT 13
AA020187
ID AA020187 standard; cDNA to mRNA; 2243 BP.
XX
XX AA020187;
AC
XX
XX 31-MAR-1992 (first entry)
DT
XX
XX Soybean seed stearyl-ACP desaturase coding sequence from pds1.
DE
XX
XX soya bean; plant oil; stearic acid; ss.
XX
XX Glycine max strain Cultivar Wye.
OS
XX
XX Key Location/Qualifiers
FH
```

```

FT 5'UTR 1..69
FT /tag= a
FT transil_peptide 70..165
FT /tag= b
FT /note= "putative"
FT mal_peptide 166..1242
FT /tag= c
FT 3'UTR 1240..2243
FT /tag= d

XX MO9118985-A.
XX 12-DEC-1991.
XX
XX 16-MAY-1991; 91MO-US03288.
XX
XX 25-MAY-1990; 90US-0529049.
XX
XX (DUPO ) DU PONT DE NEMOURS CO.
XX
XX Hitz WD, Yadav N;
XX
XX WPI; 1992-007469/01.
XX
XX P-PSDB; AAR20011.
XX
XX DNA encoding soybean stearyl-ACP desaturase enzyme and precursor
XX - and chimeric genes, for plant transformation and control of
XX levels of satd. and unsaturated fatty acids in edible oils
XX
XX Claim 1; Page 54; 70pp; English.
XX
XX A Lambda ZAP cDNA library was prepared from soybean embryos polyA RNA
XX and used to infect E.coli B84 cells. The cells were plated and
XX transfected to nitrocellulose filters for hybridisation. Probes were
XX designed based on the N-terminal amino acid sequence of purified
XX stearyl-ACP desaturase. Six positive plaques were subjected to
XX plaque purification and the regions of each vector comprising the
XX cDNA inserts were excised. The resulting phagemids were used to
XX infect E.coli XL-1 Blue cells to give 6 double-stranded plasmids
XX pBS1 to pBS6. There was a common 0.7kb BglII fragment found in the
XX desaturase gene of all 6 plasmids. The invention covers chimeric
XX genes comprising nucleotides 1-2243, 70-1245 or 166-1245 of this
XX sequence, linked to suitable control sequences. They are used for
XX transforming oil-producing plant cells to produce antisense inhibition
XX of desaturase in the seed, overexpress precursor desaturase in the
XX cell plastid or express mature enzyme, respectively.
XX See also AAQ20188-Q20190 and AAR20012.
XX
XX Sequence 2243 BP: 625 A; 447 C; 528 G; 643 T; 0 other:
XX
XX Query Match 38.8%; Score 521.2; DB 13; Length 2243;
XX Best Local Similarity 68.5%; Pred. No. 2.6e-136;
XX Matches 743; Conservative 0; Mismatches 324; Indels 18; Gaps 1;
XX
OY 112 CCAGTGCACGAGTTCAGTTCCTCCAGGCTTTCATGCGTTCACATCTCACTCC 171
DB 118 CAAATGCCAGCTCCAGATCTCCCGCTTCGCGATGGCTTCACCCCTCCGCTCC 177
OY 172 ATGTTCTTGAATATCTCAAAAGTCCGCCA-----ATCTTCAATC 213
DB 178 AAGAGGTTGAAATATTTAGAGGATTCCTCCAGAGAACTGCATGTTCAAGTA 237
OY 214 ACTCACTATAGCCACCCCAAAAGCTAGAAATATTCACCTCCCTGATGTTGGCTAGG 273
DB 238 ACCCACTCATGCTCCCGCAGAAATTTGAGATTTTCAATCTTTGGAGATTTGGCTGAC 297
OY 274 AACATGTGTTATTCACCTCAAAATCTGCGAAATCTTGGCAACACAGACTACTTG 333
DB 298 CAGAACATCTTACCTACCTTAACCTGTAGAAATATTTGGCAACACAGAGATTTTAA 357
OY 334 CCGGATCCGCTGCAGACAGCTTCGAGAGCAAGTCCGGAGCTTGGGGAAGAGCGCANG 393
DB 358 CCGGACCCCTCTCTCAGATGATTTTGAAGAGCAAGTAGGAAGTGAAGAGAGCAAG 417

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OY 394 GAGATTCGCCGACACTATTTTGTGCTTACGTTGAGATATGATTCACAGAGACACTT 453
DB 418 GAGATTCGAGATGATTTACTTTGTTCTTGTGCGAGACATGATTCACAGAGAGCTCTG 477
OY 454 CCACATATATGTCATTGCTCATATAGTGTGATGATTAAGATATAGACTGGGCTGAG 513
DB 478 CTTACTTACCAAACTATGTTAAATCTTGGATGAGTGTGATGATGAACAGGTCACAGC 537
OY 514 CCCAGTGTGGGCAATGTGAGTACAGTACGAGCTGCGAAGAGATAGATGAGTGTGAC 573
DB 538 CTTACTTCTGCGCAATTTGGACAAAGGCAATGAGCTGCTGAGAAACACAGCAGTGTAT 597
OY 574 CTTTCGAATTAAGTACCTTATTTGTCTGGAAGGCTTGATAGAGAAATTTGAGAAAGACT 633
DB 598 CTTCTTAACAAATATCTGTACTTGTAGTGTGAGCGAGTTGACATGAACAAATTTGAGAGACA 657
OY 634 ATTCAATATCTCATCGGCTCAGCAATGATATCAAGTCAGAAACAGCCCTTACTAGGC 693
DB 658 ATTCAGTACCTTATTTGGTGTGGATGATCCTCGAGACCGAAGACCCCTTACTGTGGT 717
OY 694 TTGATCTACACATCTTCCACAGAGAGAGCAACCTTCATATCCCATGCGCAACAGCCAG 753
DB 718 TTGATTTTACACTTTCATTTCAAGAGAGGCAACCTTATATCCACGGAACACGCGCAGG 777
OY 754 CTGGCCCAACACTTACGCGCAGCAAGAACTCTGCTACATCTGCGCTCCATCGCCTCGAC 813
DB 778 CTTGCGAAGAGAGATGTTGACATAAAATTTGGCACAGATCTGCGGCAATGTCCTCAGAT 837
OY 814 GAGAGCGCCACGACCCACAGCTTACACCAAGATCTGTGGAAGAAAGCTCCGTCAGATCGAC 873
DB 838 GAGAAACGCGCCAGACGATGATACACAAAGATAGTGAAGAAAGCTGTTGAGTGTCTCT 897
OY 874 GACACACAGATTAATCTTTCAGATATGATGCGCAAAATTAACATATGCGCAGCGAC 933
DB 898 GATGTCACATTTATGTCATTTTCCGACATGATATGAGAAAGATTTGCTATGCCAGCAC 957
OY 934 TTGATGTACGAGCAAGTGAAGCAACTTCTTTTAAACATTTCAACGCGCTTGTCTCAGAGA 993
DB 958 CTTATGTATGACGCGCGCGCAGCAACCTGTTGATTAACACTCTGCGCGCGCAGCGC 1017
OY 994 GTGNGGCTTATTTCTCCGTTGATTTATGCGACATCTTACATCTTTCGCGGATTAATG 1053
DB 1018 ATTTGGGCTTACCTCTCAAGGACTATGCTGACATCTCTGAATTTGTTGGGAGAGCTG 1077
OY 1054 AATGTGAAAGGCTTACGCGGCTGTGCGACGAGGCGCAAAAGCGCAGATATGTGTGT 1113
DB 1078 AAGGTGAGCAGCTTAACCGGACTTTCAAGTGAAGGGAAGAAAGGCTCAGGAATACGTTGT 1137
OY 1114 GAATTTGGTCCCAAGATTTAGCGAGTGAAGAGAAAGTGCAGGGGGAAGAGAAAGAAAG 1173
DB 1138 GGGCTGCCACCAAGATTCAGAAAGTTGGAGAGAGAGCTCAACGAGCAAGAGAGAGTGTG 1197
OY 1174 AAMGC 1178
DB 1198 TCAAC 1202

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RESULT 14
AAV29236
ID AAV29236 Standard; cDNA to mRNA; 2243 BP.
XX
XX AAV29236;
XX
XX 21-AUG-1998 (first entry)
XX
XX Nucleotide sequence of the soybean seed stearyl-ACP desaturase.
XX Soybean stearyl ACP-desaturase gene; chimeric gene; antisense;
XX transformation; saturated fatty acid; unsaturated fatty acid;
XX soybean oil; inhibition; polyunsaturate; monosaturate; ss.
XX
XX Glycine max.
OS

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XX Key Location/Qualifiers
FH 5' UTR 1..69
FT /*tag= a
FT CDS 70..1245
FT /*tag= b
FT /product= "soybean seed stearyl-ACP desaturase"
FT transit_peptide 70..165
FT /*tag= c
FT mat_peptide 166..1245
FT /*tag= d
FT 3' UTR 1246..2243
FT /*tag= e
XX
XX US5760206-A.
XX
XX 02-JUN-1998.
XX
XX 07-JUN-1995; 95US-0474587.
XX
XX 07-JUN-1995; 95US-0474587.
XX 19-MAY-1991; 91WO-US03288.
XX 11-DEC-1992; 92US-0995657.
XX
XX (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
XX Hiltz WD, Perez-Grau L, Yadav NS;
XX WPI: 1998-332247/29.
XX P-PSDB; AAW37939.
XX
XX Nucleic acids encoding soybean seed stearyl-ACP desaturase enzyme -
XX are useful for the anti-sense inhibition of the enzyme in
XX transformed plant cells
XX
XX Claim 1: Column 37-40; 26pp; English.
XX
XX This is the nucleotide sequence of the soybean stearyl
XX ACP-desaturase gene, used in the method of the invention, which
XX involves the creation of chimeric genes which are used in (antisense
XX orientation) to transform plant cells. The nucleic acids are useful
XX for controlling the levels of (un)saturated fatty acids in soybean oil.
XX In transformed cells (seeds), the chimeric genes transcribe the
XX antisense RNA to the complementary mRNA for the enzyme. This results
XX in inhibition of expression of the endogenous enzyme and reduction in
XX desaturation of seed oil. This results in seed oil which is low in
XX saturates and polyunsaturates and high in monosaturates, giving an oil
XX which is healthier.
XX
XX Sequence 2243 BP; 625 A; 447 C; 528 G; 643 T; 0 other;
XX
XX Query Match 38.8%; Score 521.2; DB 19; Length 2243;
XX Best Local Similarity 68.5%; Pred. No. 2,6e-136;
XX Matches 743; Conservative 0; Mismatches 324; Indels 18; Gaps 1;
XX
XX 112 CCAGTGACGACGAGTTCCTCCAAAGGTTTTCATGCTTCACATCTCACTTAATCTC 171
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 118 CAAATGCCGACGCTCCCGCTCCGATGCGTTCCACACCTCCGCGTTCC 177
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 172 ATGCTTTCGATTAATCTCAAAAGTCCGCCAA-----ATCTTCAAGTC 213
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 178 AAAGAGGTTGAAATATTTAAAGACCATTCCTCCTCCAGAGAGAGTGCATGTTCAAGTA 237
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 214 ACTCACTCATGCCACCCCAAGAGTAGAATATTCAGTCCCTTGATGATTGGGCTAGG 273
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 238 ACCCACTCATGCTCCCGACAGAGATGAGATTTTCAATCTTTGAGAGATTGGCTGAC 297
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 274 AACAAATGCTGATTCACCTCAAAATCTGCGAAGAAATCTTGGCACACACAGACTGCTTG 333
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 298 CAGACATCTTGACATCATTAACCTGTAGAAAATGTTGGGCAACACAGAGATTTTAA 357
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 334 CCGGATCCGCTGTCAGACGAGATTCCAGAGCAAGTCCGGAGTTGGGGAAGAGGCGCAAG 393
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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DB 358 CCCGACCCCTCCTCAGATGATTTGAAGACGAAGTGAAGAACTGAGAGAGACCAAG 417
QY GAGATTCGCGAGACTATTTTGTGTAGTTGAGATATGATCAGAAAGACACTT 453
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 418 GAGATTCGAGATGATTTACTTTTGTCTTGTGCGAGACATATCAGAGAGAACTCTG 477
QY 454 CCACATATATGCTCTATGCTCAATAGTGTGTATTTAGCATGAGACTGGGCTGAG 513
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 478 CTTACTTACCAAACTATGTAATACTTTGATGAGATTCGATGAAGAAACAGATGCCAGC 537
QY 514 CCCAGTCTGTGGGCAATGTGACCTAGGCGATGACCTGCGAGAGATATGATGTTGAC 573
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 538 CTTACTTCTCGGCAATTTTGACAAAGGCAATGACTGCTGAGAAACAGACGCTGAT 597
QY 574 CTTCTCAATTAAGTACTTATTTGCTGTGAAGAGGTTGATATGAGAAATTTGAGAAGCT 633
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 598 CTTCTTAACAAATATCTGTACTTGTAGTGCAGATTTGACATTAACAAATTTGAGAAG 657
QY 634 ATTCATATCTCATCGGCTCAGGAATGATATCAAGTCAAGAAACAGCCCTACTAGGC 693
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 658 ATTCAGTACCTTATTTGGGCTGGGATGATCCTCGACCGAGAAAGACGCCCTACTGCT 717
QY 694 TTTCATCTACATCTCTTCCAGAGAGAGACCACTTCATATCCATGCGCACAGCCAG 753
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 718 TTTCATTTACCTTCATTTCAAGAGAGGCAACCTTCATATCCACGGAACACGCGCAG 777
QY 754 CTGCCCCAACACTAGCGCGCAAGAACTCGCTCATCTGCGGCTCCATCCCTCCGAC 813
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 778 CTTCGGAAGACGACATGTTGATCAATTAATTTGGCACAGATCTCGCGCATTTGCTCAGAT 837
QY 814 GAGAAAGCCGACGCGCACAGCTTACACCAAGATCTGTGGAAGAACTCGCTTACATCCAGCC 873
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 838 GAGAAAGCCGACGAGAGACTGCTCATACCAAGATATGGAAGAACTGTTGAGTTGATCCT 897
QY 874 GACACACAGTAAATGCTTTGAGATATGATGACGCAAAATAACAATGACGCGCAC 933
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 898 GATGTTACAGTTATGCTATTTGCTCCACATGATGAGAAAGATTTGCTATGCCAGACAC 957
QY 934 TTGATGTCAGCAGAGATGACGAATCTTTTAAACATTTTACAGGCGGTTGCTCAGAGA 993
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 958 CTTATGATAGACGCGCGCGACGACACCTGTTGATTAATCTCTCCGCGCGAGCCG 1017
QY 994 GTGNGGTTTATTTCTGCTGTTGATTTTGCACATTTAGAGTTTGTGTGGAATAAG 1053
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1018 ATTTGGGTTTACCTGCAAGAGACTATGCTGACATCTCAATTTTGTGTGGAGAGTGG 1077
QY 1054 AATGTGAAGGCTTTACGGGCTGTGCGACGAGGCGGCAAAAGCGCAGGAATATGTGT 1113
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1078 AAGGTGACAGACTTAACGCGACTTTCAAGTGAAGGAAAGGCTCAGGAATACGTTGT 1137
QY 1114 GAATTGGGTTCCCAAGATTTAAGCGAGTGAAGAGAAAGTCCAGGGGCAAGAGAAAGAA 1173
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DB 1138 GGGCTTCCCAAGAAATTCAGAGGTTGGAGAGAGGCTCAAGCAAGAGCAAGAGTGG 1197
QY 1174 AAAGC 1178
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DB 1198 TCAAC 1202
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RESULT 15
AAND2378 standard; CDNA: 1553 BP.
ID AAND2378;
AC AAND2378;
XX
XX 12-FEB-2002 (first entry)
XX
XX Cotton stearyl-ACP delta9-desaturase (ghsABD-1) protein CDNA.
XX Cotton; delta9-desaturase; fatty acid delta12-desaturase; palmitic acid;
XX linoleic acid; stearic acid; oleic acid; transgenic plant;
XX cotton seed oil; stearyl-ACP delta9-desaturase; SAB-1; ss.
XX
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 1, 2002, 21:12:16 ; Search time 3483 Seconds

(without alignments)
11230.023 Million cell updates/sec

Title: US-09-732-597-1

Perfect score: 1344
Sequence: 1 caaccaccagaataataaat.....tttgagtttaaglaaaaaa 1344Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

1: gb_da.*

2: gb_htg.*

3: gb_in.*

4: gb_cm.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vl.*

15: em_da.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vl.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htg_mus.*

34: em_htg_pln.*

35: em_htg_frod.*

36: em_htg_mam.*

37: em_htg_vrt.*

38: em_sy.*

39: em_htgo_hum.*

40: em_htgo_mus.*

41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	613.4	45.6	1297	6	A74271	A74271 Sequence 1
2	613.4	45.6	1309	8	I12944	I12944 Sequence 1
3	613.4	45.6	1309	8	COVACIACI	M93115 Coriander
4	573.8	42.7	1643	8	RCCSACPD	M59857 Ricinus com
5	572	42.6	1662	8	RCSIEA	X56508 R.communis
6	572	42.6	1668	6	I90191	I90191 Sequence 15
7	564.4	42.0	1580	8	SSMSACPD	D42086 Sesame mRNA
8	550	40.9	1194	8	SIN31331	M59858 Cucumis sat
9	537.4	40.0	1407	8	CUSMSACPD	AF051134 Macfadysen
10	533	39.7	1509	8	AF051134	AF051134 Thunbergia
11	526.8	39.2	1319	8	TA007552	M83199 Stimonidia
12	524	39.0	1576	8	SMMSCP	AF172728 Arachis h
13	523.8	39.0	1548	8	AF172728	I16556 Sequence 32
14	522	38.8	1533	6	I16564	I19664 Sequence 12
15	522	38.8	1533	6	I90189	I90189 Sequence 12
16	522	38.8	1533	6	CMSACPD	M61109 C.linctori
17	522	38.8	1533	6	I13990	I13990 Sequence 1
18	521.2	38.7	1524	6	A74273	A74273 Sequence 3
19	520	38.7	1524	6	BNSACPD	X63364 B.napus mRN
20	520	38.7	1524	8	AF116861	AF116861 Persea am
21	515.4	38.3	1517	8	LUSACPD	X70862 L.usitatiss
22	514.2	38.3	1447	8	AF395441	AF395441 Arabidops
23	513.2	38.2	1206	6	AR195536	AR195536 Sequence
24	513	38.2	1621	6	GHSACPD	X95988 G.hinsutum
25	512.6	38.1	1495	6	I90194	I90194 Sequence 19
26	511.8	38.1	1495	6	BRSACPD	X60978 B.rapa cv.R
27	511.6	38.1	1206	8	AY094014	AY094014 Arabidops
28	511.6	38.1	1623	8	SOVSACPD	L34346 Glycine max
29	511.6	37.1	1711	8	AY048233	AY048233 Arabidops
30	511.6	37.1	1516	8	BNAACPD	X97325 B.napus mRN
31	508.2	37.8	1622	8	ATSPACPD	X93461 A.thaliana
32	506.6	37.7	1768	8	SCSACPD	X78833 S.commerson
33	506.4	37.2	1653	8	AY056428	AY056428 Arabidops
34	499.8	37.2	1185	8	AY090324	AY090324 Arabidops
35	499.8	37.2	1493	8	OE058141	OE058141 Olea europ
36	498.4	37.1	1567	8	AY088096	AY088096 Arabidops
37	498.4	36.9	1279	8	AY128883	AY128883 Arabidops
38	495.8	36.9	1583	8	AY099784	AY099784 Arabidops
39	495.8	36.9	1583	8	AY087294	AY087294 Arabidops
40	493.4	36.7	1337	8	TA007597	TA007597 Thunbergia
41	493.2	36.7	1335	8	HA091339	HA091339 Helianthus
42	493.2	36.7	1507	8	POTSACPD	M91238 Solanum tub
43	489.6	36.4	1426	8	HA091340	HA091340 Helianthus
44	489.6	36.4	1426	8	HAN242632	HAN242632 Helianthu
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ALIGNMENTS

RESULT 1

A74271

LOCUS A74271 1297 bp DNA linear PAT 15-OCT-1999

DEFINITION Sequence 1 from Patent W09401565.

ACCESSION A74271

VERSION A74271.1 GI:6064296

KEYWORDS

SOURCE

ORGANISM

Coriander.
Coriandrum sativum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; eusterids II; Apiales; Apiaceae; Coriandrum.
REFERENCE
1 (bases 1 to 1297)
MURPHY, D.J. and FAIRDAIRN, D.J.
GENES FOR ALTERING PLANT METABOLISM

Db 781 AAATCGTGAGAGAGCTTCCGAGATTCAGCACACCACTGTATTCGCAATTTCTGAC 840
QY 901 ATGATGCGCAAAAAATATACATTCGCCAGGCACTTGATAGACGAGAGTCAAGACTT 960
Db 841 AAGATGAGGAAGAAATAATAGCAATGCCAGCTCATGCAATGTAGAGGGCTCCGATGATG 900
QY 961 CTTTAAACATTCACGGCGGTGTCTCAGAGAGTNGGGTTATTCCTCGTTGATTA 1020
Db 901 CTTTCAAGCACTTCACAGCCGTGTCTCAGCAGATTTGGAGTCTACTCTCATGAGATTAC 960
QY 1021 TCGCAGATCTTACAGTTCTGTGTGATAAATGGAATGTGGAAGGCTTACGGGGCTGTG 1080
Db 961 TGTGACATTAATTTCTGTGTGATAAATGGAATGTGGAAGGCTTACGGGGCTGTG 1020
QY 1081 GAGCAGGGGCGGAAAGCGAGGAATATGTGTGATTTGGGTCCCAAGATTCAGCGAGTG 1140
Db 1021 GGTGAAGGAGGAAGGCTCAAGAAATATGTTGTAGCTTGGCTGTAGATCAGAGAGATT 1080
QY 1141 GAAGAGAAAGTGCAGGGGAGAGAGAAAGAAAGCTAGACCCCTTTCTTTTCAG 1200
Db 1081 GAGGAGAAAGTTCAAGGCAAGG-----AGAGAAAGCTGTGTGTGCTGTGGCTTTACAG 1134
QY 1201 TGGATTTTCAATCGGAGCTTGAAGATATGA 1230
Db 1135 TGGATTTTCAACCGCTCAGATCATCATATGA 1164

RESULT 4

LOCUS

RCCSACPD 1643 bp mRNA linear PLN 22-AUG-1995
RCCSACPD Ricinus communis stearyl-acyl-carrier protein desaturase mRNA, 3'

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

POBMED

FEATURES

source

Location/Qualifiers
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/organism="Ricinus communis"
/db_xref="taxon:3988"
/tissue_type="seed"
/dev_stage="developing"
-1..1239
/codon_start=1
/product="stearyl-acyl-carrier protein desaturase"
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/db_xref="GI:951427"
/translation="FRÖTTKNKKKVRKTKMALKNLPISÖTOKLPSFALPPMASTRS
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OYLISGMDPRTENSPYLGFIYTSFOERATFISHGNTAQAHEGDIKLAOICGTAA
DEKRHETAVTKIVEKLEIFEDPDGTVLAFAFDMARKKISMAHLMYGRDNLEPESAV
AORUGVYTAADADLLEPLVGRKVKDKLTGLSABEGKADYICRPLPRIRLREERAG
RAKEAPTWPFESWIFRÖVKL"

CDS

BASE COUNT 462 a 321 c 383 g 477 t
ORIGIN
Query Match 42.7%; Score 573.8; DB 8; Length 1643;
Best Local Similarity 67.3%; Pred. No. 6.6e-129;
Matches 869; Conservative 0; Mismatches 393; Indels 30; Gaps 3;

QY 10 AAAATAAAAATAAACTCAGAGAGAAGAAAGAAATGGCTTTGAAGCTCAATTTCCAA 69
Db 13 ACAAATAACCAAAAGAAAAAGTAAGAAAAAACAATGGCTCTCAAGCTCAAT---CGT 69
QY 70 TGCAGAGAACCAACCCCTGCGTTGCTAAGTCAACCATTTACAGATGACAGATTAC 129
Db 70 TTTCTTTCAAAACCAAAAGTAACCTCTTTCGCTTCCACCAATGGCCAGTACCA 129
QY 130 TCTCCAAAGGTTTTCATGGCTTCACACTGCACTCACTCACTCACTGGTCTGATATTC 189
Db 130 TCTCCAAAGTCTTACATGGCTCTTACCTCACTCACTCACTGGTCTGATATTC 189
QY 190 AAAAGTCC-----GCCAAATCTTCAAGTCACTCACTCACTCACTCACTCACT 231
Db 190 AAGAACCTTTTCATGGCTCTGCGGAGGATACATGTTCAAGTTACCATTTCTATGCCACCC 249
QY 232 CAAAGCTAGAAATATTCAGATCCCTTGTATGATGGGCTTACAGACAATGTGTTATTCAC 291
Db 250 CAAAGATTTGAGATCTTTAAATCCCTTACCAATTTGGGCTGAGAGAACATTTGGTTTCA 309
QY 292 CTCGAATCTGTGAGAAATCTTGGCAACCAAGTCACTTGTCCGATCCGGATCCGCTGACAG 351
Db 310 CTGAGCCAGTTGAGAAATGTTGGCAACCGAGAGATTTTTCGCAAGATCCCGCTCTGAT 369
QY 352 GATTCGAGAGGCAAGTGGGAGATTGAGGAAAGGCGCAAGAGATTCGCCAGCATAT 411
Db 370 GATTTGATGAGAGCAAGTCAAGGCAACTCAGGAGAGAGCAAAAGAGATTCCTGATGATTA 429
QY 412 TTTGTGGTGTAGTTGAGATATGATCAGAGAAAGACATTCACATATATGTATG 471
Db 430 TTTGTGTGTGTGTGTGAGATGATGAGAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 489
QY 472 CTCGAATGAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 531
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QY 532 TGGACTAGGGCATGAGCTGCGGAGAAAGAAATGAGATGATGATGATGATGATGATGATGATG 591
Db 550 TGGCAAGGCGCATGAGCTGCGGAGAAAGAAATGAGATGATGATGATGATGATGATGATGATG 609
QY 592 TATTTGTCTGGAAGGTTGATATGAGAGAAATTTGAGAGGCTTTCATATCTCATCGCG 651
Db 610 TACCTTCTGAGAGAGTGGACATGAGGCAAAATTTGAGAGGCTTTCATATCTCATCGCG 669
QY 652 TCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 711
Db 670 TCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 729
QY 712 CAAGAGAGAGCACTTCATATTCATATCCATGCCACAGACAGCCAGCTGGCCACACTACGCG 771
Db 730 CAGGAAAGGCGCACTTCATATTCATATCCATGCCACAGACAGCCAGCTGGCCACACTACGCG 789
QY 772 GACAAGACCTGCTCAGATCTGCGGCTCCATGCGCTCCGAGAGAGAGGCGCCAGCGCACA 831
Db 790 GACATTAAGTTGGCTCAAAATATGTGTACATTTGTGCAATTTGTGCAATTTGTGCAATTTGT 849
QY 832 GCTTACACCAAGATCGGAGAAAGCTGCTGAGATGAGACCCGACACACAGTATTTGCT 891
Db 850 GCTTACACCAAGATGAGGAGAAAGCTTTTGAATTTGATTTGATTTGATTTGATTTGATTTG 909
QY 892 TTTGCAATATGATGCGCAAAAAAATAACATGCGCAGCGCATTTGATGTACGAGCAAGT 951
Db 910 TTTGCTGATATGATGAGAAAGAAATTTTATCTCTGCAACTGATGATGATGATGATGATG 969
QY 952 GAGCACTTCTTTTAAACATTTTCACGGGGTGTCTCAGAGAGAGGAGGAGGAGGAGGAGGAG 1011
Db 970 GATGATTAATCTTTTTCACCTTTTCAGCTGTGCGAGGCTCTTGAGATCTACACAGCA 1029
QY 1012 TTTGATTAATGAGCACTTATGAGATTTCTGTGTGATTAATGAGATGAGATGAGATGAGATGAG 1071
Db 1030 AAGGATTAATGAGCACTTATGAGATTTCTGTGTGAGGAGATGAGATGAGATGAGATGAGATG 1089

[illegible]

	Best Local Similarity	69.1%	Pred. No. 1.8e-128;	
	Matches	823;	Conservative	0;
			Mismatches	341;
			Indels	27;
			Gaps	2;
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	111			
Db	89	ACCATTGGCCAGTACCAGATCTCCCTTAATTTCAATGGCGCTCAACCTCAAGTCTGGTTC	148	
OY	171	CATGGTTCTTGATATATCTCCAAAAGTCC-----GCCAAATCTTCAAGT	212	
	171			
Db	149	TAAAGAGTTGTGAGATATCTCAAGAAAGCCCTTTCATGCTCTCCGGAGGATCATTTGTTCAGGT	208	
OY	213	CACTCACCTATGGCACCCCAAAAGCTGAATAATTCAGATCCCTGTATGATGGGGCTAG	272	
	213			
Db	209	TATCCATTCTATGGCCACCCCAAAAGATTGAATCTTTAAATCCCTAGACAAATTTGGGCTGA	268	
OY	273	GAACAAATGTGTTGATTTACCTCAATCTGTGTGAGAAATCTTGGCAACCAACAAGACTACTT	332	
	273			
Db	269	GGAGAAACATTTCTGGTCTACTGTGAACCCAGTTGAGAAATGTTGGCAACCGCAGATTTT	328	
OY	333	GCCGGATCCGGTGTTCAGAGGATTCGAGAGCAACATGCCGGAGTTGAGGAAAGGCCAA	392	
	333			
Db	329	GCCAAATATCCCGCTGTGTGATTTGATGACCAAGTCAAGGACACTCAGGAGGAGAGCAAA	388	
OY	393	GGAGATTTCCCAACGACTATTTTGTGTGTCTTAACTTGAATATGATACAGAAAGAACACT	452	
	393			
Db	389	GGAGATTTCTGTATGATTTTGTGTTTGTGTTGGTGGAAACATGATTAACGAAAGACCTT	448	
OY	453	TCCAACTATATATGTATATGCTCAATAGGTGTGATGATGATTAAGGTAGACTGGGCTGA	512	
	453			
Db	449	TCCCACTTATCAACAACATGCTGATATCTTGGATGATCTGGGATGGAACAGGTGCAG	508	
OY	513	GCCCACTCTTGGGCAATGTGACTAGGGCATGTGACTGCCGAAGAGAAATAGACATGTGA	572	
	513			
Db	509	TCCCTACTCTTGGGCAATTTGGCAAGGGCATGTGACTGCCGAAGAGAAATAGACATGTGA	568	
OY	573	CCTTCTCAATATAGTACCTTTATTTGTCTGTGGAAGGTTTATATGAGAAATTTGAGAAGAC	632	
	573			
Db	569	CCTCTCTCAATATAGTATCTCTACTATCTGTGAGCAAGTGTGACATGAGCGAAATTTGAGAAAC	628	
OY	633	TATTTCAATATTCATCGGCTCAGGAATGTGATATCAATGACAAAACACGCCCTTCACTAGG	692	
	633			
Db	629	AATTTCAATATTTGATTTGGTTCAGGAATATGATATCCAGGACAGAAACAGTCCATATCTTTGG	688	
OY	693	CTTCTATACACATCTCTTCCAAAGAGAGCAACCTTCTATCTCCATGTCCAACACAGCCAA	752	
	693			
Db	689	GTTCTATATATCATTCATTTCCAGGAAGAGGCAACCTTCTATCTCATGTGGAAACACTGCCCCG	748	
OY	753	GCTGGCCCAACACTATGCGCGACACAGAACCTGCTACATCTGCGGCTTCCATGCGCTCCGA	812	
	753			
Db	749	ACAACCCAAAGAGCATGTGAGACATATAAGTTGGCTCAAAATATGTGTATCAATTTGCTGCAGA	808	
OY	813	CGAGAAAGGCCACGGCCACAGGCTACACCAAGATCGTGGAAAAGCTCGGTGATGTGACCC	872	
	813			
Db	809	TGAGAAAGGCCATGAGACACAGCTACACCAAGATATGTGAAAACACTCTTGTGATTTGATCTCC	868	
OY	873	CGACACAACAGTAAATTTGCTTTTGCAGATATATATGCGCAAAAAAATTAACATGTCCAGCGCA	932	
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OY	933	CTTGTATGTACAGCGAAGTGAACACTTCTTTTAAACATTTACGGCGGTTTCTCAGAG	992	
	933			
Db	929	CTTGTATGTATGATGCGCAGATGATAACTTTTGGACCACTTTTCAGCTGTGTCGACACCG	988	
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	1113			

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Db	1164	-----GAAACACCACCAATGCTTTCAGCTGGATTTTTCATAGGCAAGTGAAGT	1219
Qy	1233	AGGAAGGAGAGGAATGGAGGAGCAAAATGAGTGTGATTTCTATATGC	1293
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ACCESSION	190191		PAT 10-AUG-1998
VERSION	190191.1	GI:3410131	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 1668)		
AUTHORS	Thompson, G.A. and Knauf, V.C.		
TITLE	Plant desaturases - compositions and uses		
JOURNAL	Patent: US 5723595-A 15 03-Mar-1998;		
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BASE COUNT	464 a 325 c 386 g 493 t		
ORIGIN			
Query Match	42.6%;	Score 572;	DB 6; Length 1668;
Best Local Similarity	69.1%;	Pred. No. 1.8e-128;	
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Db	89	ACCAATGGCCAGTACCAAGATCTCTAAGTTCTACATGSCCTCACCTCAAGCTGTGTC	148
Qy	171	CATGGTTCTGATTAATCTCAAAAGTCC-----GCCAATCTTCAGT	212
Db	149	TAAAGAAAGTGAAGATCTCAAGAAGCTTTTCAATGCTCCCGGAGAGTACATTTGAGG	208
Qy	213	CACCTACTTATGCCACCCCAAAAGCTAAGATATTTCAAGTCCCTTGATGATTTGGGCTAG	272
Db	209	TACCCATTTCTATGCCACCCCAAAAGATTGAGATCTTTAAATCCCTAGACAATTTGGCTGA	268
Qy	273	GAACATGTGTTGATTCACCTCAATCTGTGCGAATCTTTGGCAACACAGACTACTT	332
Db	269	GGAGAACATTTCTGCTTCACTGAGCAATGTGGAATATGTGGCAACCGAGATTTT	328
Qy	333	GCCGATCCGGTGTCAAGCGATTGAGAGCAAGTCCGGAGTTAGAGGAAGGGCCAA	392
Db	329	GCAGATCCCGCTCTGATGATTTATGATGAGCAAGTCAGGGAAGTCAAGGAGAGACAA	388
Qy	393	GGAGATTTCCGAGACATTTTGTGTTAGTTAGTTGAGATATGATCAGACAAAGACACT	452
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Qy	453	TCCACATATATGTCTATGCTCAATAGTGTGATTTAAGATGACATGGGGCTGA	512
Db	449	TCCACTTATCAAAACATGCTGAATACCTTGATGAGTTCGGGATGTAACAGGTGCAAG	508
Qy	513	GCCCATGCTTGGGCAATGTGCACTAGGCGATGAGTCCGGAAGAGATATGATGGTGA	572
Db	509	TCTTACTTCTTGGGCAATTTGGACAAGGGATGAGCTCGCGAAGAGATATGATGGTGA	568
Qy	573	CCCTTCAATTAATACCTTATTTGATCGAAGGGTTGATATGAGGAATTTAGAGAAC	632
Db	569	CTCTCTCAATAAAGATATCTTACCTATCTGAGACGATGAGCATGCGCAATTTGAGAAC	628
Qy	633	TATTCATATATCTCATGGGCTCAGGAATGATATTCAGTCAAGAAACAGCCCTTACTAGG	692

D6	AATTCAATATTGTTAGTTCGAGAAATGCATCCAGCAGCAAGAAAACAGTCCATACCTTG6	688
OY	CTTCACTTACACAATCCTTCCAGAAGAGAGAACACTTTCATATATCCCATGCCAAGCACAA	752
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D6	ACAAGCCAAAGAGATGGAGACATAAAGTTGGCTCAATATGTGGTAACAATTGCTGCAGA	808
OY	CGAAGAGCGCCACGCCACGACCTACACCAAGATCGTGAAGAAAGCTCGCTCAGATCGACC	872
D6	TGAAAGAGCGCATATAGACAGCGCTACCAAAAGATGTGGAAAAAACTCTTTAGATTTGATCC	868
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D6	TCTTGAGATCTACACAGCAAGATTTATGACGATRTATTTGAGCTTCTTGGGGCACAATG	1048
OY	GAAATCTGGAAGAGGCTTACGAGGGCTGTGCGACAGAGGGCGGCAAAAGCGAGATATGTGTG	1112
D6	GAAAGTGTGATTAACATTAACGAGGCTTTGAGCTGAGGGAGCAAAAGGCTCATATGTTTTG	1108
OY	TGAATTTGGGTTCCCAAGATTAGSCCGAGTGGAAAGACAAGATCGAGGGAAGGAAAGAA	1172
D6	TGCGTTACTCTCCAGAAATTAGAAGCTGGGAAGAGAGACTTCAAGAAAGGCGCAAG--	1163
OY	GAAAGCTCAGACACCCCTGTTTCTTCAGCTGGATTTTCATCGGAGTGTGAAGATATGAC	1232
D6	---GAAACACCCACCATTCCTTTTACGCTGGATTTTTCATAGGCAAGTAGAGCTGTAAGT	1219
OY	AGGAAGGGAAGAGGAAATGAGAGACCAATAGCTGTAGTATGTTCTATATGTC	1283
D6	GGCTTAAGTGCAGCGCAACCGAATGTTAGTTTCTCTTTTTCATGTC	1270
RESULT 7		
SMSACPD	1580 bp	linear
LOCUS		PLN 01-FEB-2000
DEFINITION	Sesame mRNA for stearyl-acyl carrier protein desaturase, complete cds, clone CDS01.	
ACCESSION	D42086	
VERSION	D42086.1	GI:575941
KEYWORDS	stearyl-acyl carrier protein desaturase.	
SOURCE	Sesamum indicum (strain:4294) seed, cDNA expansion stage cDNA to mRNA, clone lib:lambdla gtl10 clone:CDS01.	
ORGANISM	Sesamum indicum	
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Lamiales; Pedaliaceae; Sesamum.	
AUTHORS	1 (bases 1 to 1580)	
TITLE	Yukawa,Y., Takaiwa,F., Shoji,K., Masuda,K. and Yamada,K.	
JOURNAL	Structure and expression of two seed-specific cDNA clones encoding stearyl-acyl carrier protein desaturase from sesame, Sesamum	
MEDLINE	indicum L.	
REFERENCE	Plant Cell Physiol. 37 (2), 201-205 (1996)	
AUTHORS	96213006	
JOURNAL	2 (bases 1 to 1580)	
TITLE	Yamada, K.	
FEATURES	Direct Submission	
SOURCE	Submitted (12-NOV-1994) Kyoto Yamada, Toyama University, Faculty of Science, Biology; Gofuku 3190, Toyama, Toyama 930, Japan (E-mail:yamada@sci.toyama-u.ac.jp, Tel.:0764-41-1271(ex.2335), Fax:0764-41-2972)	
	Location/Qualifiers	
	1..1580	

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RESULT 8
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Lamiales; Pedaliaceae; Sesamum.
1 (bases 1 to 1194)
Chopra, V.L.
Transgenic expression of cDNA encoding steroyl acyl carrier protein
desaturase of sesamum indicum in indian mustard
Unpublished
2 (bases 1 to 1194)
Chopra, V.L.
Transgenic indian mustard high in oleate
Unpublished
3 (bases 1 to 1194)
Kantar, S.
Direct Submission
Submitted (20-JUN-2001) Kanrar S., Nrcpb, Iari, 15, NRCPB, IARI,
New Delhi, 110012, INDIA
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Oy 401 CGGACACATATTTTGGGTGTTAGTTGGAGATTTGATCAGAGAAAGCAATTCACAT 460
Db 494 CGATGAGAGTACTTGGTGGTTTATGTTGAGAGACATGATTAAGAGAAAGCCCTTCACATT 553
Oy 461 ATATGCTATGCTCAATGATGATGATGATTAATTAAGATGAGACTGGGCGTGCAGCCAGTG 520
Db 554 ACCAGACATGCTGATTAATTTGATGATGATGATGATGATGATGATGATGATGATGATG 613
Oy 521 CTTGGGCAATGTGAGTACGATGATGATGATGATGATGATGATGATGATGATGATGATG 580
Db 614 CTTGGGCAATGTTGACAAAGGCTTGGATGATGATGATGATGATGATGATGATGATGATG 673
Oy 581 ATTAAGTACCTTATTTGCTGGAAGGCTTGAATTAAGAGAAATTTGAGAGACTTATTCAT 640
Db 674 ATTAATATCTTTTACCTATCTGAGAGAGTGCAGATGAGAGAGGTTGAGAAACAAATTCAGT 733
Oy 641 ATCTCATGCGCTCAGAGATGATGATTAAGTCAAGAAACAGCCCTTACCTTACCTATCT 700
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RESULT 10
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LOCUS AF051134
DEFINITION Macfadyena unguis-catl acyl-ACP desaturase (fad1) mRNA, complete
cds
ACCESSION AF051134

VERSION AF051134.1 GI:2944443
KEYWORDS Macfadyena unguis-catl.
SOURCE Macfadyena unguis-catl.
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Lamiales; Bignoniaceae; Macfadyena.
REFERENCE 1 (bases 1 to 1509)
AUTHORS Cahoon,E.B., Shah,S., Shanklin,J. and Browse,J.
TITLE A Determinant of Substrate Specificity Predicted from the Acyl-ACP Desaturase of Developing Doxantha Seed
JOURNAL Plant Physiol. (1998) In press
2 (bases 1 to 1509)
AUTHORS Cahoon,E.B., Shah,S., Shanklin,J. and Browse,J.
TITLE Direct Submission
JOURNAL Submitted (25-FEB-1998) IBC, Washington State University, Pullman, WA 99164-6340, USA
FEATURES
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BASE COUNT 416 a 357 c 357 g 379 t
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Best Local Similarity 67.6%; Pred. No. 5,7e-119;
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Oy 85 CCTGCTCGTTTCTTAAGTACCATTTACAGTGCAGAGTTAGCTCCAAAGGTTTC 144
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Oy 145 ATGGCTTCACTGTCAACTCTAACCTCCATGCTTGTGATTAATCTCAAA----- 193
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Qy	970	1029			Arachis hypogaea
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Qy	1030	1089			Arachis hypogaea
Db	1103	1162			Arachis hypogaea
Qy	1090	1149			Arachis hypogaea
Db	1163	1222			Arachis hypogaea
Qy	1150	1209			Arachis hypogaea
Db	1223	1273			Arachis hypogaea
Qy	1210	1269			Arachis hypogaea
Db	1274	1333			Arachis hypogaea
Qy	1270	1306			Arachis hypogaea
Db	1334	1370			Arachis hypogaea

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Db	95	CTTCTCTTCATCGTTCTCGCTTCTCTCAATGGCTAGCTCGATCTCCAAAGTTCCGCA	154	
QY	146	TGGCTTCCACTGTCAACTCTAACTCCATGGTCTTGATTAATCTCAAAAGTCC-----	197	
Db	155	TGGCTTCCACCTCCCGCACTGGTTCAAAAAGAGTTGAATAATCTCAAGAAGCCCTTCACGC	214	
QY	198	-----GCCAATCTTCAAGTACTACTGTATGCCACCCCAAAAAGCTAGAAATAT	247	
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QY	248	TCAAGTCCCTTATGTATGTTGGCTAGGAACATGTGTGTTATTCACCTCAATCTGTACGAA	307	
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QY	308	AATCTTGGCAACCAAGCATCTACTTGC CGGATCCGGTGTCAAGCGAGTTGAGAGCAAG	367	
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QY	368	TTCGGGAGCTTGAAGGAAAGGCGCAAGAGATTCGCGAGCAATTTTGGTGTTGGTG	427	
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QY	548	CTGCCAAGAGATATAGCATGTGGACCTTCTCAATAGTACCTTTATTTGTCTGGAAGG	607	
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QY	608	TTGATATGAGAAATTTGAGAGACTATTCATATCTCATCGGCTCAGAGATGGAATATCA	667	
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QY	668	AATCGAAAAAGCCCTTCCACTAGGCTTATCTATACATCCCTTCCAAAGAGAGCAACT	727	
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QY	848	TGGAAGAAGTCCGTGAGATCGACCCGACACACAGTAAATTTGCTTTGCAGATATGATGC	907	
Db	875	TGAGAGAGCTTTTGAGATCGATCTGATGAACTGTAATGAGCTTTTTCGACATGATGA	934	
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QY	968	AACATTTACGGGCGTGTGTCAGAGAGTGGGGTTTATTTCTGCTTGGATTTATTTGACAA	1027	
Db	995	AAACATTTTCTGCGCTGCGCTCAGCGCATCGAATCTTCAATCGCAAGGATATGCGTATA	1054	
QY	1028	TCTTAGAGTTTCTGTGTGATAAATGGAATGTGSAAGAGCTTACGGGGCTGTGGAGAGG	1087	
Db	1055	TCCTTAATTTTCTTGTGGCCCGGTGGAAGGTGGCAGACCTTAACCGGACTCTGCTGTCAG	1114	
QY	1088	GCGGAAGAGCGAGGAATATGTGTGAATTTGGTCCCAAGATTAGCGGAGTGAAGAGA	1147	

Dd	1115	GAAAGGAAAGCTCAGATTTATGTTCCTCCGGTGCCTCAAGAATCCGAAGATTCCGAAGCG	1174
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DEFINITION	Sequence 32 from patent US 5475099.		linear PAT 03-Apr-1996
ACCESSION	I16556		
VERSION	I16556.1 GI:1251464		
KEYWORDS	.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified. 1 (bases 1 to 1533)		
AUTHORS	Knauf,Y.C. and Thompson,G.A.		
TITLE	Plant fatty acid synthases		
JOURNAL	Patent: US 5475099-A 32 12-DEC-1995;		
FEATURES	Location/Qualifiers 1..1533 source /organism="unknown"		
BASE COUNT	420 a 327 c 392 g		394 t
ORIGIN			

Query Match:	38.8%	Score 532:	DB 6:	Length 1533:
Best Local Similarity:	68.5%	Pred. No. 2.7e-116:		
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Db	301	CCACCACAGAAAGATAGAGATTTTCAAAATCCATCGAGGGTTGGCGTAGACAGAACTATTG	360
OY	286	ATTCACTCAAAATCTGTGGAGAAATCTTGGCACACAGACTACTTCCGGATCCGGTG	345
Db	361	GTTCACCTAAAGCCAGTGGAGAAATGTTGGCAGACAGACTTCTTCCCGGACCTTCCA	420
OY	346	TCAGACGGATTGCGAGACAGAGTGGGGAGTTGAGGAGAAAGGGCCCAAGAGATTCCGCAC	405
Db	421	TCTGAAGATTTGATGAACAMGTCAAGGAACTAAGGGCAAGACCAAGAGATTTCTGAT	480
OY	406	GACTATTTTGTGCTTATAGTTGAGATATGATCACAGAAAGCACTTCCACATATATG	465
Db	481	GATTTACTTTGTTGTTTGGTGGATATGATTATACAGAAAGCCCTACACTTACCA	540
OY	466	TCTATGCTCAATAGTGTGTGATGCTTTTAAGATGAGACTGGGGCTGAGCCCAAGTCTGG	525
Db	541	ACAATGCTTAATACCTTAGATGCTGTACGTGTGAGACTGGGGCTTAGCCTTAGCGCTTGG	600
OY	526	GCAATGTGAGTACAGGCAATGCACTCCGACAGAGAAATAGACATGATGACCTTCTCAATAG	585
Db	601	GCTGTCTGGACTAGGGCTTGGACACTGGAAGAACAGACAGCATGGCGATCTTCTCCACAC	660
OY	586	TACCTTTATTTTCTCTGGAAGGTTGATATTTAGAGAAATTTAGAGACATATTCATATCTC	645
Db	661	TATCTTACTACCTTTCTGGGGGGGTAGACATGAGGCGAGATACAGAAACAATTCAGTATCTC	720
OY	646	ATCGGCTCAGAAATGATATCAAGTCAGAAAAACACCCCTACCTAGGGCTCACTTACACA	705
Db	721	ATTGGGTACAGAAATGATCTCTGTACCGAAAAAGCCCTTACCTTGGGTTCACTTACACA	786
OY	706	TCTTTTCAGAGAGACAACCTTCATATTCATTCGCAACAGCCAAAGCCAGCCCGCCACAC	765

Db	781	TCGTTCAAGAGCGTGCACATTTTGTTCCTCAGSAAACCGCGCACGATGCAGAAAGAT	840
Qy	766	TACGGCGACAAGAACCTCGCTCACATCTCGGGCTTCATCGCTCCGACGAGAGCGCCAC	825
Dp	841	CATGGCGACGTGAACCTCGCGCAAAATTTGTGTACAAATCGCGTGTGACGAAAGGCTCAC	900
Qy	826	GCCACAGCCCTACCCAGATCGTGGAAAAAGCTCGCTGATGTGACCCCGACACAAACAGTA	885
Dp	901	GAGACCGCTTATACAAAGATAGTCGAAAAAGCTATTCGAGATCGATCTCGATGGCACCGTT	960
Qy	886	ATTGCTTTTGCAGATATATATCGCCAAAAAAATTAACATGCCAGCGCACTTATGTAGCAC	945
Dp	961	CTTGCTTTTGGCGACATATAGGAAAAAGATCTCGATGCCCGCGCACCTGATGTAGCAT	1020
Qy	946	GSAACTGACGAACTCTTTTAAACATTTTCACGGCGGTTGCTCAGAGTGNGGTTTAT	1005
Dp	1021	GGGCGTGTATGACAAACCTCTTGGAACATTTTCGGGGGTTGGCCAAAGACTCGGGCTTAC	1080
Qy	1006	TCTCGGTTGGATTTATTTGGCAGATCTTAGAGTTTCGGTGGATTAATGGAATGTGGAAAG	1065
Dp	1081	ACCGCAAAAGACTACCGCGACACTACTGCAATTTTGTGTGGGGCGGTGGAAAGATGGCGAT	1140
Qy	1066	CTTACGGGGGCTGTGCGACGAGGGCGGCAAAAGCGCAGATAATGTGTGAATTTGGGTC	1125
Dp	1141	TTGACCGGCTATCTGTGTGMAAGGGCGTTAAAGCGCAAGATTATGTTGGGGTTGCCACCA	1200
Qy	1126	AAGATTAGCGAGTGGAGAGCAAAAGTGCAGGGGGAAGGAAGAGAAAGACTGAGCAC	1185
Dp	1201	AGAATCAAGAGCTGAGAGAGAGACACTCAAGGCGCAGCAAG-----GAAGGACCT	1251

Db 1252 GTGTTCATTCAGCTGATTTTCATAGACACGGTGAAGCTGGAACAAAAAACAAGC 1310

LOCUS	119664	1533 bp	DNA	linear	PAT 07-OCT-1996	
DEFINITION	Sequence 32 from patent US 5510255.					
ACCESSION	119664					
VERSION	119664.1	GI:1600019				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	Unclassified.					
AUTHORS	1 (bases 1 to 1533)					
TITLE	Knauf, V.C. and Thompson, G.A.					
JOURNAL	Plant fatty acid syntheses					
FEATURES	Patent: US 5510255-A 32-23-APR-1996;					
	Location/Qualifiers					
	1..1533					
source	/organism="unknown"					
BASE COUNT	420 a	327 c	392 g	394 t		
ORIGIN						
Query Match	38.8%; Score 522; DB 6; Length 1533;					
Best Local Similarity	68.5%; Pred. No. 2.7e-16;					
Matches 739; Conservative	0; Mismatches 331; Indels 9; Gaps 1;					
OY 166	AAC	TGATG	ATATCTCA	AAAGTCG	CGCAAAATCTCTCAAGTCACTCACTATG	225
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	1	1	1	1	1	1
Db 241	AATG	CAAGAA	GCCCTTTTCA	CACTCCAGAGAGTTCATGTTCA	GTCAGTACGACACTCCATG	300
OY 226	CAAC	CCCAAA	AGCTAAGAAATATTTCA	GTGCTCTGATGATTTGGCTAGGAACAAATGTGTTG	285	
	1	1	1	1	1	1
	1	1	1	1	1	1
Db 301	CCAC	CAAGAA	GATATGATTTTCAAAATCCATCGAGGGTTGGCTGACACAACTATTATG	360		
OY 286	ATTCA	CTCAATATCTGTGAGAAATCTTG	GGCAATCTTGCGCAACCAAGACTACTTGGCCGATCCGGTG	345		
	1	1	1	1	1	1
	1	1	1	1	1	1
Db 361	GTTCA	CTTAAGCCAGTGTGAGCAAAATGTTGGCAAGCACACAGATTTCTTGCCGACCTTCA	420			
OY 346	TCAG	ACGATTCGAGAGCAAGTGGGAGATTG	AGGAAAGGCCAAGAGATTCCGAC	405		
	1	1	1	1	1	1
	1	1	1	1	1	1

Db 421 TCTGAGGATTTGATGACAAAGTCAAGGAACTAAGGCCAAGCAAGAGATTCCTGAT 480
QY 406 GACATATTTTGTGGCTTGTATGAGATATGATCAGAGAAAGCACTTCCACATATATG 465
Db 481 GATTAATTTTGTGGTGTATGAGATATGATCAGAGAAAGCCCTACTACTATACCA 540
QY 466 TCTATGCTCAATAGGTGTATGAGATATGAGAACTGGGGCTGAGCCCAAGTCTTG 525
Db 541 ACAATGCTTAATACCTAGATGTGTAGCTGATGAGACTGGGGCTAGCCTTAGCCCTTG 600
QY 526 GCAATGTGAGTGAAGGCACTGACTCGGCAAGAAATAGACATGTGACCTTCTCAATAG 585
Db 601 GCTGTCTGAGTGAAGGCTGAGACAGCTGAGAAACAGAGATGCGATCTTCTCCACAC 660
QY 586 TACCTTATTTGTCTGGAAGGTTGATGAGAAATGAGAAAGCTATTCAATATCTC 645
Db 661 TATCTTACTTCTTGTGGGGGTAGACATGAGGCAATACAGAAAGCAATTCAGTATCTC 720
QY 646 ATCGGCTCAGGAATGATATCAAGTCAAGAAACAGCCCTACTAGGCTTCACTACACA 705
Db 721 ATTTGGTCAAGGAATGATCTCTACGAAACAGCCCTTACCTTGGTTCATCTACACA 780
QY 706 TCTTTCAGAGAGAGACCACTCATATCCATGCGCAACAGGCAAGCTGCGCAACAC 765
Db 781 TCGTTTCAGAGGCTGCCACATTTGTTCTCAGGAAACACCGCAGGCAATGCAAAAGAT 840
QY 766 TACGGGACAAAGACCTGCTCAATCTGCGGCTCCATGCGCTTCGACGAGAGAGCCAC 825
Db 841 CATGGGACGTAAGCTGCGCAATTTGTGTACAAATCGGCTCTGACGAAAGCGTCAC 900
QY 826 GCCACACCTTACACCAAGATCTGGAAGCTGCTGAGATCGACCCGACACACAGTA 885
Db 901 GAGACCCCTTATACAAAGATAGTGAAGATATTCAGATCGATTCCTGATGCGACCGTT 960
QY 886 ATTGCTTTGAGATATGATCGCAAAATAAACAATGCCAGCGCACTTGATGACGAC 945
Db 961 CTTCCTTTGCGCATGATGAGAAAGATTCGATGCCGACACTTGATGATGAT 1020
QY 946 GGAAGTGAAGACTCTTTTAAACATTTCAAGCGGCTTGTGCTCAGAGAGTNGGTTAT 1005
Db 1021 GGGCGTGTATGACAACTCTTGAACATTTCTGCGGGTGTGCCAAGACTCGCGCTTAC 1080
QY 1006 TCTGCGTTGATTTTGGACATCTTAGAGTTTCTGTGATTAATGGAATGTGGAAGG 1065
Db 1081 ACCGCCAAAGACTACGCCGACATCTGGAATTTCTGTGCGGCGGTGGAAGTGGCGAT 1140
QY 1066 CTTACGGGCTGTGAGAGAGGGGCAAAAGCGCAAGATATGTGTAATTTGGTCCC 1125
Db 1141 TTGACCGGCTATCTGTGTAAGGGCGTAAAGCGCAAGATTATGTTTGGGTTGCCACCA 1200
QY 1126 AAGATTAGGCGGTGAGAGAAAGTGCAGGGGAAGAGAAAGCAAGCAAGCTGAGCAC 1185
Db 1201 AGAATCAGAGAGCTGAGAGAGAGACTCAAGGGCGAGCAAG-----GAAAGACCT 1251
QY 1186 CTTGTTTCTTTCAGCTGATTTTCAATCGGAGTTGAAGATATGAACAGAGAGGGAAG 1244
Db 1252 GTTGTTCATTCAGCTGATTTTCATAGCACAGTGAAGCTGTGAAGAAAAAAGG 1310

Search completed: December 1, 2002, 23:59:59
Job time : 3492 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 1, 2002, 21:18:46 ; Search time 35 Seconds

(without alignments)
2319.502 Million cell updates/sec

Title: US-09-732-597-2

Perfect score: 2062
Sequence: 1 MALKINFOCKKNHPAFAKS.....KKAEHPVSFSWTFRELKI 394

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1457	70.7	396	10	Q43140
2	1446	70.1	396	10	Q43141
3	1441	69.9	396	10	Q9SEK6
4	1424	69.1	396	10	Q93X20
5	1401.5	68.0	401	10	Q39355
6	1395	67.7	396	10	Q24497
7	1391.5	67.5	401	8	Q9XOR7
8	1384.5	67.1	409	10	Q9SW87
9	1381.5	67.0	401	10	Q22832
10	1381.5	67.0	401	10	Q94AE9
11	1381	67.0	396	10	Q24498
12	1377	66.8	396	10	Q9M4N5
13	1371	66.5	396	10	Q65040
14	1370.5	66.5	396	10	Q8S059
15	1365	66.2	358	10	Q43196
16	1365	66.2	396	10	Q82014

17	1363	66.1	396	10	Q9SBA2	Q9SBA2
18	1359.5	65.9	396	10	Q43197	Q43197
19	1356	65.8	396	10	Q9M879	Q9M879
20	1355	65.7	396	10	Q8VXJ8	Q8VXJ8
21	1355	65.7	396	10	Q8VXJ7	Q8VXJ7
22	1353.5	65.6	399	10	Q947F1	Q947F1
23	1347.5	65.3	407	10	Q42591	Q42591
24	1338	64.9	390	10	Q43198	Q43198
25	1320.5	64.0	394	10	Q9LFF04	Q9LFF04
26	1262.5	61.2	386	10	Q947F2	Q947F2
27	1247.5	60.5	411	10	Q9M881	Q9M881
28	1223.5	59.3	401	10	Q9LFF05	Q9LFF05
29	1221	59.2	384	10	Q9XFC1	Q9XFC1
30	1220	59.2	396	10	Q9M880	Q9M880
31	1197	58.1	374	10	Q9MAR6	Q9MAR6
32	1174.5	57.0	368	10	Q40879	Q40879
33	1171.5	56.8	385	10	P92933	P92933
34	1106	53.6	387	10	Q41510	Q41510
35	831	40.3	222	10	Q64906	Q64906
36	635	30.8	161	10	Q9XFH1	Q9XFH1
37	609.5	29.6	167	10	Q43142	Q43142
38	295	14.3	328	16	Q9XAL3	Q9XAL3
39	271.5	13.2	338	16	Q50050	Q50050
40	256.5	12.4	338	16	Q8VKD4	Q8VKD4
41	256.5	12.4	338	16	Q50824	Q50824
42	153	7.4	170	2	Q9K539	Q9K539
43	142.5	6.9	828	12	Q9WRP6	Q9WRP6
44	135	6.5	275	16	Q9X793	Q9X793
45	122.5	5.9	2269	5	Q26223	Q26223

ALIGNMENTS

RESULT 1
ID Q43140 PRELIMINARY; PRT; 396 AA.
AC Q43140;
DT 01-NOV-1996 (TREMREL. 01, Created)
DT 01-NOV-1996 (TREMREL. 01, Last sequence update)
DT 01-JUN-2002 (TREMREL. 21, Last annotation update)
DE Acyl-[acyl-carrier protein] desaturase precursor (EC 1.14.99.6)
DE (Stearoyl-ACP desaturase).
OS Sesamum indicum (Oriental sesame) (Gingelly).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Lamiales; Pedaliaceae; Sesamum.
OX NCBI_TaxID=4182;
RN [1]
RP SEQUENCE FROM N.A.
RC SPRAIN-4294;
RX MEDLINE=96213006; PubMed=8665096;
RA Yukawa Y., Takaiwa F., Shoji K., Masuda K., Yamada K.;
RT "Structure and expression of two seed-specific cDNA clones encoding
RT stearyl-acyl carrier protein desaturase from sesame, Sesamum indicum
RT L.";
RL Plant Cell Physiol. 37:201-205(1996).
CC -1- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A
CC CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL
CC CHAIN (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: STEAROYL-[ACYL-CARRIER PROTEIN] + AH(2) + O(2)
CC -1- COFACTOR: OLEOYL-[ACYL-CARRIER PROTEIN] + A + 2 H(2)O.
CC -1- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH (BY
CC SIMILARITY).
CC -1- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY
CC ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE
CC OILS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
DR EMBL, D42086; BAA07681.1; -.
DR HSSP; P22337; 1AFR.
DR InterPro; IPR005067; FA_desat.

DR InterPro: IPR001225; FA desaturase.
 DR Pfam: PF03405; FA desaturase.2; 1.
 DR PROSITE: PS00574; FATTY-ACID-DESATUR.2; 1.
 KW Chloroplast; Fatty acid biosynthesis; NADP; Oxidoreductase;
 KW Transf. peptide.
 FT TRANSIT 34 33 POTENTIAL.
 FT CHAIN 1 396 STEAROYL-ACYL CARRIER PROTEIN DESATURASE.
 SO SEQUENCE 396 AA; 45168 MW; A23475AB676A0940 CRC64;

Query Match 70.7%; Score 1457; DB 10; Length 396;
 Best Local Similarity 69.5%; Pred. No. 4,2e-104;
 Matches 280; Conservative 50; Mismatches 57; Indels 16; Gaps 4;

OY 1 MALKL---NFQCKKNHPAPAFKSPDPVTRVSSPRVMASTVNSNVLDMLKSPN----53
 DB 1 MALKLAINFQSKCPSPFLP---PVASVRSKFFMASTLRSGSKVEVTKRPFNPRE 56
 OY 54 --LQVTHSMPPQKLEIFKALSDMARNVLIHLKSVESKMPQDYLDPVSDGFEEOYREL 111
 DB 57 VHVQVTHSMPPQKLEIFKALSDMARNVLIHLKSVESKMPQDYLDPVSDGFEEOYREL 116
 OY 112 RERAKETPDYFVVLGDMTEERLPTYSMLNRCGDKETGAEPSAMAMTRAWTAEE 171
 DB 117 RERAKETPDYFVVLGDMTEERLPTYSMLNRCGDKETGAEPSAMAMTRAWTAEE 176
 OY 172 NRHGDLLNKLYLSGRVDMRKIEKTIQYLLIGSGMDIKSENSPYLGITYTSFOERATFISH 231
 DB 177 NRHGDLLNKLYLSGRVDMRKIEKTIQYLLIGSGMDIKSENSPYLGITYTSFOERATFISH 236
 OY 232 ANTKLAQHYGDKNLAIHICGSIASDEKRNATYKIVEKIAEIDPDTVIAFADMRKKI 291
 DB 237 GNTARLARHEDDLKLAQICGTIADDEKRNATYKIVEKIAEIDPDTVIAFADMRKKI 296
 OY 292 TMPRLMYDGSDELFFKFTVAQVRYXSALDYCDLLEFLVDKNVRLTGLSDEGRKA 351
 DB 297 SMPRLMYDGRDNLFFHSSVAQRLGVTAKDVADLLEHIVARKVANLTGLSADGRKA 356
 OY 352 QEYVCELGPKIRVREKYGKKEKKKAHPVSFWIFNREIKI 394
 DB 357 QDYVCELGPKIRVREKYGKKEKKKAHPVSFWIFNREIKI 396

RESULT 2
 ID 043141 PRELIMINARY; PRT: 396 AA.

AC 043141;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Acyl-[acyl-carrier protein] desaturase (EC 1.14.99.6) (Stearoyl-ACP desaturase).
 OS Sesamum indicum (Oriental sesame) (gingerly).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Lamiales; Pedaliaceae; Sesamum.
 OX NCBI_TaxID=4182;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=4294;
 RA Yukaawa Y., Takaiwa F., Yamada K.;
 RT "Structure and expression of two cDNA clones encoding stearyl-acyl carrier protein desaturase in sesame."
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL CHAIN (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: STEAROYL-[ACYL-CARRIER PROTEIN] + AH(2) + O(2) = OLEOYL-[ACYL-CARRIER PROTEIN] + A + 2 H(2)O.
 CC -1- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH (BY SIMILARITY).
 CC -1- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE OILS.

CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
 DR EMBL: D49832; BAA08635.1; -.
 DR HSSP: P22337; IAFR.
 DR InterPro: IPR005067; FA-desat.
 DR InterPro: IPR001225; FA-desaturase.
 DR Pfam: PF03405; FA desaturase.2; 1.
 DR PROSITE: PS00574; FATTY-ACID-DESATUR.2; 1.
 KW Chloroplast; Fatty acid biosynthesis; NADP; Oxidoreductase;
 KW Transf. peptide.
 SO SEQUENCE 396 AA; 45212 MW; 1335DEC4A1B2BF9A CRC64;

Query Match 70.1%; Score 1446; DB 10; Length 396;
 Best Local Similarity 69.2%; Pred. No. 2,9e-103;
 Matches 279; Conservative 49; Mismatches 59; Indels 16; Gaps 4;

OY 1 MALKL---NFQCKKNHPAPAFKSPDPVTRVSSPRVMASTVNSNVLDMLKSPN----53
 DB 1 MALKLAINFQSKCPSPFLP---PVASVRSKFFMASTLRSGSKVEVTKRPFNPRE 56
 OY 54 --LQVTHSMPPQKLEIFKALSDMARNVLIHLKSVESKMPQDYLDPVSDGFEEOYREL 111
 DB 57 VHVQVTHSMPPQKLEIFKALSDMARNVLIHLKSVESKMPQDYLDPVSDGFEEOYREL 116
 OY 112 RERAKETPDYFVVLGDMTEERLPTYSMLNRCGDKETGAEPSAMAMTRAWTAEE 171
 DB 117 RERAKETPDYFVVLGDMTEERLPTYSMLNRCGDKETGAEPSAMAMTRAWTAEE 176
 OY 172 NRHGDLLNKLYLSGRVDMRKIEKTIQYLLIGSGMDIKSENSPYLGITYTSFOERATFISH 231
 DB 177 NRHGDLLNKLYLSGRVDMRKIEKTIQYLLIGSGMDIKSENSPYLGITYTSFOERATFISH 236
 OY 232 ANTKLAQHYGDKNLAIHICGSIASDEKRNATYKIVEKIAEIDPDTVIAFADMRKKI 291
 DB 237 GNTARLARHEDDLKLAQICGTIADDEKRNATYKIVEKIAEIDPDTVIAFADMRKKI 296
 OY 292 TMPRLMYDGSDELFFKFTVAQVRYXSALDYCDLLEFLVDKNVRLTGLSDEGRKA 351
 DB 297 SMPRLMYDGRDNLFFHSSVAQRLGVTAKDVADLLEHIVARKVANLTGLSADGRKA 356
 OY 352 QEYVCELGPKIRVREKYGKKEKKKAHPVSFWIFNREIKI 394
 DB 357 QDYVCELGPKIRVREKYGKKEKKKAHPVSFWIFNREIKI 396

RESULT 3
 ID 09SEK6 PRELIMINARY; PRT: 396 AA.

AC 09SEK6;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Acyl-[acyl-carrier protein] desaturase (EC 1.14.99.6) (Stearoyl-ACP desaturase).
 OS Persea americana (Avocado).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Persea.
 OX NCBI_TaxID=3435;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. FUERTE;
 RA Madl L., Prusky D.;
 RT "Sequence of a cDNA Clone Encoding an Avocado (Persea americana) (delta9)- Stearoyl-Acyl Carrier Protein Desaturase (Accession No. AF116861)." (PGR99-167).
 RL Plant Physiol. 121:1054-1054(1999).
 CC -1- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL CHAIN (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: STEAROYL-[ACYL-CARRIER PROTEIN] + AH(2) + O(2) = OLEOYL-[ACYL-CARRIER PROTEIN] + A + 2 H(2)O.
 CC -1- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH (BY

```

CC SIMILARITY).
CC -I- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY
CC ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE
CC OILS.
CC -I- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -I- SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).
CC -I- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
DR EMBL: AF116861; AAF15308.1; -.
DR HSSP: P22337; IAFR.
DR InterPro: IPR005067; FA_desat.
DR InterPro: IPR001225; FA_desaturase.
DR Pfam: PF03405; FA_desaturase.2; 1.
DR PROSITE: PS00574; FATTY_ACID_DESATUR_2; 1.
KW Chloroplast; Fatty acid biosynthesis; NADP; Oxidoreductase;
KW Trans peptide.
SQ SEQUENCE 396 AA; 45454 MW; 0F971ABDC07C2AD7 CRC64;

Query Match 69.9%; Score 1441; DB 10; Length 396;
Best Local Similarity 67.6%; Pred. No. 7,1e-103;
Matches 273; Conservative 55; Mismatches 53; Indels 24; Gaps 6;

QY 1 MALKLNFOCKKHPAAFAKSPPLV-----TRVSSPRVFMASTVNSNVLNLKSPN---SP 51
DB 1 MALKLS-----PYMFOGQKLPFLASPPSNLRSRPRVMASTLRSTKEVDNIKKPSP 53
QY 52 P---NLQVTHSNPPOKLEIFKSLDDMARNNVLHLKSVKSWQPODYLPDPVSDGFEQY 108
DB 54 PREHVQVTHSNPPOKLEIFKSLDDMARNNVLHLKSVKSWQPODYLPDPVSDGFEQY 113
QY 109 RELRRAREIPDDYFVVLGDMTEALPTYSMLNRCGIDEGAEPSANAMTRAWT 168
DB 114 ELRLRAAEIPDDYFVVLGDMTEALPTYSMLNRCGIDEGAEPSANAMTRAWT 173
QY 169 AEENHGDLLNLYLGLSGVDMRKIEKTYOYLIGSGMDIKSENSPYLGFITYSFOERATF 228
DB 174 AEENHGDLLNLYLGLSGVDMRKIEKTYOYLIGSGMDIKSENSPYLGFITYSFOERATF 233
QY 229 ISHAATAKLAQHYGDKNLAHICGSIASDEKRRHATATKIVEKLAETDPTTYIAFDMMRK 288
DB 234 ISHGATARAQKYGDDKLAKICGTIAADEKRHEATATKIVEKLEFDIDPDTYIAFDMMRK 293
QY 289 KITTPAHLMYDGSDELLEFKHFTAAVQRYVXSALDYCDLLEFLVDMKMMVERLTGLSDG 348
DB 294 KITSPAHLMYDGDQDDLEFGHFSSVAORLGVYAKDYADILEFLVAKMMVERLTGLSPDG 353
QY 349 RKAQYVCELGPKIRVEEKVOGKEKKKAEPH-VSFSWIFNRELKI 394
DB 354 KTAQEFICKLAPRIRSLERARSRAK---EGPTIPFSWIFNREVKL 396

RESULT 4
Q93X20 PRELIMINARY; PRT; 396 AA.
ID 093X20:
AC 093X20:
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Stroyl acyl carrier protein.
OS Sesamum indicum (Oriental sesame) (Gingelly).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Lamiales; Pedaliaceae; Sesamum.
OX NCBI_TaxID=4182;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=DEVELOPING SEED;
RA Kanrar S.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=DEVELOPING SEED;
RA Chopra V.L.;
RT "Transgenic expression of cDNA encoding steroyl acyl carrier protein

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RT desaturase of sesamum indicum in Indian mustard.";
RN Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=DEVELOPING SEED;
RA Chopra V.L.;
RT "Transgenic indian mustard high in oleate.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ313331; CAC44792.1; -.
DR InterPro: IPR005067; FA_desat.
DR InterPro: IPR001225; FA_desaturase.
DR Pfam: PF03405; FA_desaturase.2; 1.
DR PROSITE: PS00574; FATTY_ACID_DESATUR_2; UNKNOWN.1.
SQ SEQUENCE 396 AA; 45054 MW; 4945DFAC687BB2 CRC64;

Query Match 69.1%; Score 1424; DB 10; Length 396;
Best Local Similarity 67.7%; Pred. No. 1,5e-101;
Matches 273; Conservative 53; Mismatches 61; Indels 16; Gaps 4;

QY 1 MALKL--NFQCKNHPAAFAKSPPLVTRVSSPRVFMASTVNSNVLNLKSPN---SP 53
DB 1 MALKLAINFQSPKCSFALP---PVASVSPKPFVASTLRSGSKREVTVRKPPNPRE 56
QY 54 --LQVTHSNPPOKLEIFKSLDDMARNNVLHLKSVKSWQPODYLPDPVSDGFEQYREL 111
DB 57 VHVQVTHSNPPOKLEIFKSLDDMARNNVLHLKSVKSWQPODYLPDPVSDGFEQYREL 116
QY 112 REKAKETIPDDYFVVLGDMTEALPTYSMLNRCGIDEGAEPSANAMTRAWTAE 171
DB 117 REKAKETIPDDYFVVLGDMTEALPTYSMLNRCGIDEGAEPSANAMTRAWTAE 176
QY 172 NRRGDLNLYLGLSGVDMRKIEKTYOYLIGSGMDIKSENSPYLGFITYSFOERATFISH 231
DB 177 NRRGDLNLYLGLSGVDMRKIEKTYOYLIGSGMDIKSENSPYLGFITYSFOERATFISH 236
QY 232 ANAKLAQHYGDKNLAHICGSIASDEKRRHATATKIVEKLAETDPTTYIAFDMMRK 291
DB 237 GNTARLAREHGDKLALQICGTIAADEKRHEATATKIVEKLEFDIDPDTYIAFDMMRK 296
QY 292 TTPAHLMYDGSDELLEFKHFTAAVQRYVXSALDYCDLLEFLVDMKMMVERLTGLSDG 351
DB 297 SMPAHLMYDGRDNDLDPHFSSVAORLGVYAKDYADILEFLVAKMMVERLTGLSAGQKA 356
QY 352 QQYVCELGPKIRVEEKVOGKEKKKAEPHVSFSWIFNRELKI 394
DB 357 QDVYCGLPRIIRLERRAQRKAQAP---KIPPSWVHREVLQ 396

RESULT 5
Q93935 PRELIMINARY; PRT; 401 AA.
ID 093935:
AC 093935:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Acyl-[acyl-carrier protein] desaturase (EC 1.14.99.6) (Stearoyl-ACP
DE desaturase).
GN B4.
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. JET NEUF;
RC MEDLINE=94286739; PubMed=8016261;
RX Slocumbe S.P., Piffanelli P., Fairbairn D., Bowra S., Hatzopoulos H.,
RX Tsiantis M., Murphy D.J.;
RT "Temporal and tissue specific regulation of a Brassica napus stearyl-
RT acyl carrier protein desaturase gene.";
RL Plant Physiol. 104:1167-1176(1994).
CC -I- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A

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CC eurousids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3707;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PUSA JAIRISAN;
RA Vageshabu H.S., Kirtl P.B., Chopra V.L.;
RT "Nucleotide sequence of the coding region of the plastidic delta-9-
stearoyl-acyl-carrier protein desaturase of Brassica juncea.";
RL Submitted (MAY-1999) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A
CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL
CHAIN (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: STEAROYL-[ACYL-CARRIER PROTEIN] + AH(2) + O(2)
= OLEOYL-[ACYL-CARRIER PROTEIN] + A + 2 H(2)O.
CC -1- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH (BY
SIMILARITY).
CC -1- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY
ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE
OILS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
DR EMBL: AF153420; AAD40245.1; -
DR HSSP: P22337; IAFR.
DR InterPro: IPR005067; FA_desat.
DR InterPro: IPR001225; FA_desaturase.
DR Pfam: PF03405; FA_desaturase_2; 1.
DR PROSITE: PS00574; FATTY ACID DESATUR_2; 1.
KW Chloroplast; Fatty acid biosynthesis; NADP; Oxidoreductase;
KW Transit peptide.
SQ SEQUENCE 401 AA; 45504 MW; 1726DA29DCF00EB CRC64;
Query Match 67.5%; Score 1391.5; DB 8; Length 401;
Best Local Similarity 64.9%; Pred. No. 4.7e-99;
Matches 266; Conservative 58; Mismatches 61; Indels 25; Gaps 5;
QY 1 MALKL-----NFQCKNHPAFAKSP--LPVTVSSPRVEMASTVNSMVLNLSKS 50
DB 1 MALKLNPASQPYNEPSSARPPISFRSPKFLCLASSSP-----ALSSPKEVESLKK 54
QY 51 P-----PNIQVTHSMPOKLEIFKSLDDMARNNVLIHLKSVESKQPODYLPDPVSQGF 104
DB 55 PPTPKVHVQVLSMPQKLEIFKSMEDMAEONLTHLKDEKSMQPODLPDPASDGF 114
QY 105 EGVRELRERAKELPDYFVVLVGDMTTEALPTYMSMLNRCGDIKDEGAPSAAMWT 164
DB 115 EDQVKELERARELPDQYFVVLVGDMTTEALPTYQTMINTLDGVRDEGASPTMAVWT 174
QY 165 RAMTAENRRHGDLLNKYLYLSGRVDMRKIEKTYOYLIGSGMDIKSENSPYLGIYTSFOE 224
DB 175 RAMTAENRRHGDLLNKYLYLSGRVDMRKIEKTYOYLIGSGMDPTENNPNYLGFIYTSFOE 234
QY 225 RATEFSHANTAKLAQHGYGDKNLAHICGSIASDEKRHATATYTKLEAIEDDPTVIANA 284
DB 235 RATEFSHANTAKLAQHGYGDKNLAHICGSIASDEKRHATATYTKLEAIEDDPTVIANA 294
QY 285 DMRRKKTTPAHMLVYDSDELFEKHTFAVAQRYVYSALDYCDILEFLVDMKNVRLTGL 344
DB 295 DMRRKKTTPAHMLVYDSDELFEKHTFAVAQRYVYSALDYCDILEFLVDMKNVRLTGL 354
QY 345 SDEGRKAOEYVCELGPRIKRVYEVQGEKKKAHPVVSFWIFNRELKI 394
DB 355 SDEGRKAOEYVCELGPRIKRVYEVQGEKKKAHPVVSFWIFNRELKI 401
RESULT 8
Q9SM87 PRELIMINARY; PRT; 409 AA.
AC Q9SM87;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Acyl-[acyl-carrier protein] desaturase (EC 1.14.99.6) (Stearoyl-ACP

DE desaturase).
OS Arachis hypogaea (Peanut).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurousids I; Fabales; Fabaceae; Papilionoideae; Aeschynomeneae;
OC Arachis.
OX NCBI_TaxID=3818;
RN [1]
RP SEQUENCE FROM N.A.
RC Tate P.L., Koebert G., Abbott A.G.;
RT "The phylogenetic relationship of the cultivated peanut (Arachis
hypogaea L.) to its wild relative based upon comparisons of stearoyl-
ACP desaturase sequences.";
RL Submitted (JUL-1999) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A
CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL
CHAIN (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: STEAROYL-[ACYL-CARRIER PROTEIN] + AH(2) + O(2)
= OLEOYL-[ACYL-CARRIER PROTEIN] + A + 2 H(2)O.
CC -1- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH (BY
SIMILARITY).
CC -1- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY
ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE
OILS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
DR EMBL: AF177728; AAD4495.1; -
DR HSSP: P22337; IAFR.
DR InterPro: IPR005067; FA_desat.
DR InterPro: IPR001225; FA_desaturase.
DR Pfam: PF03405; FA_desaturase_2; 1.
DR PROSITE: PS00574; FATTY ACID DESATUR_2; 1.
KW Chloroplast; Fatty acid biosynthesis; NADP; Oxidoreductase;
KW Transit peptide.
SQ SEQUENCE 409 AA; 46810 MW; 7C80926BD8534A58 CRC64;
Query Match 67.1%; Score 1384.5; DB 10; Length 409;
Best Local Similarity 66.3%; Pred. No. 1.7e-98;
Matches 274; Conservative 51; Mismatches 65; Indels 23; Gaps 7;
QY 1 MALKL-----FQCKNHPAFAKSP--LPVTVSSPRVEMASTVNSMVLNLSKSP 51
DB 1 MALKLNPSPQKLEIFSSSSSSSSSSSSSSFLPQASLRSPRFMASTLRGSKSEVENLKKP 60
QY 52 -----PNIQVTHSMPOKLEIFKSLDDMARNNVLIHLKSVESKQPODYLPDPVSQGF 105
DB 61 PPTPKVHVQVLSMPQKLEIFKSLGMAEENILTLKRVESKQPODYLPDPVSQGF 120
QY 106 EGVRELRERAKELPDYFVVLVGDMTTEALPTYMSMLNRCGDIKDEGAPSAAMWT 165
DB 121 EGVRELRERAKELPDYFVVLVGDMTTEALPTYQTMINTLDGVRDEGASPTMAVWT 180
QY 166 AMTAENRRHGDLLNKYLYLSGRVDMRKIEKTYOYLIGSGMDIKSENSPYLGIYTSFOE 225
DB 181 AMTAENRRHGDLLNKYLYLSGRVDMRKIEKTYOYLIGSGMDPTENNPNYLGFIYTSFOE 240
QY 226 ATFTSHANTAKLAQHGYGDKNLAHICGSIASDEKRHATATYTKLEAIEDDPTVIANA 285
DB 241 ATFTSHANTAKLAQHGYGDKNLAHICGSIASDEKRHATATYTKLEAIEDDPTVIANA 300
QY 286 MMRRKKTTPAHMLVYDSDELFEKHTFAVAQRYVYSALDYCDILEFLVDMKNVRLTGLS 345
DB 301 MMRRKKTTPAHMLVYDSDELFEKHTFAVAQRYVYSALDYCDILEFLVDMKNVRLTGLS 360
QY 346 DEGRKAOEYVCELGPRIKRVYEVQGEKKKAHPVVSFWIFNRELKI 394
DB 361 DEGRKAOEYVCELGPRIKRVYEVQGEKKKAHPVVSFWIFNRELKI 409
RESULT 9
Q22832 PRELIMINARY; PRT; 401 AA.
ID Q22832

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AC 022832:
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Acyl-[acyl-carrier protein] desaturase (EC 1.14.99.6) (Stearoyl-ACP
DE desaturase).
GN AT2G43710 OR SS12.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons: core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Konning C.M., Koo H., Motilal K.S.,
RA Cronin L.A., Shen M., Vanaken S.E., Umayam L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT thaliana."
RL Nature 402:761-768(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Lin X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RX MEDLINE=21374454; PubMed=11481500;
RA Kachroo P., Shanklin J., Shah J., Whittle E.J., Klessig D.F.;
RT "A fatty acid desaturase modulates the activation of defense signaling
RT pathways in plants."
RL Proc. Natl. Acad. Sci. U.S.A. 98:9448-9453(2001).
CC -1- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A
CC CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL
CC CHAIN (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: STEAROYL-[ACYL-CARRIER PROTEIN] + AH(2) + O(2)
CC = OLEOYL-[ACYL-CARRIER PROTEIN] + A + 2 H(2)O.
CC -1- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH (BY
CC SIMILARITY).
CC -1- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY
CC ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE
CC OILS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
DR EMBL: AC002333; AAB64033.1; -
DR EMBL: AF395441; AAK65232.1; -
DR HSSP: P22337; IAFR.
DR InterPro: IPR005067; FA_desat.
DR InterPro: IPR001225; FA_desaturase.
DR Pfam: PF03405; FA_desaturase_2.1.
DR PROSITE: PS00574; FATTY_ACID_DESATUR_2.1.
KW Chloroplast; Fatty acid biosynthesis; NADP; Oxidoreductase;
KW Transil peptide.
SQ SEQUENCE 401 AA: 45693 MW: 0C46984578D4E1D1 CRC64;

Query Match 67.0%; Score 1381.5; DB 10; Length 401;
Best Local Similarity 65.7%; Pred. No. 2.8e-98;
Matches 266; Conservative 61; Mismatches 63; Indels 15; Gaps 6;

QY 1 MALKLNFOCKKNHPAFAKSPPLVPT-RVSSPR-VFMAST---VNSNSWVLDNLKSP----- 51
| | | | | : | | | | | : | | : : | | : : | |
DB 1 MALKRN-PLVAGQPKKFPSTRTPTPTSPRPFKFLCLASSSPALSSGPKKEVESLKKRFTTP 59
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
QY 52 --PNIQVTHSMPPQKLETKSLDDMARNNVLIHLKSVESKQWQPDYLDPPVSDGFEQYR 109
: : | | | | | : : | | | | | : | | | | | : | | | | | : | | | | |
*DB 60 REVHVOVLHSMPPQKLETKSMENNAEENLILHLKDVESKQWQPDYLDPPVSDGFEQYR 119
: : | | | | | : : | | | | | : | | | | | : | | | | | : | | | | |
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QY 110 ELERAKELPDYFVVLVGDMTTEALPTYMSMLNRCOGIKDETGAEPSSAMAMTAWTA 169
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 120 ELERARELPDDYFVVLVGDMTTEALPTYQTMINTLNDGVRDETGSPTSMAIMTAWTA 179
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
QY 170 EENRHDDLNLKTYLISGRVDMRKIEKTIQYLLSSGMDIKSENSPYLIGFYTSQERATFI 229
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 180 EENRHDDLNLKTYLISGRVDMRKIEKTIQYLLSSGMDPFRNNPYLGFYTSQERATFI 239
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
QY 230 SHNFTAKLAOHYGDKNLNIHICGSIASDEKHAATATYKIEKLAEPDPTVIAFADMMRK 289
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 240 SHNFTARQAKENHDIKLAQICGTTIADDERKHEATATYKIEKLPEDPDGIVMAFADMMRK 299
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
QY 290 KITMPAHLWYDGSDELLFKHFTAAQVRXYVSALDYCDLLEFLVDKWNERTLGLSDEGR 349
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 300 KISMPAHLWYDGRNDLFDNFSSVAQRLGYVYAKVDADLLEFLVGRWKIODTLGLSGEGN 359
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
QY 350 KAOEYCEIGPKTRVEYKQEKKKKAHPVSESMIFRREKTI 394
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 360 KAODYLGLAPRIKRIKIDERAQARAKGP---KIPFSWIHIREVOL 401
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |

RESULT 10
Q94AE9 PRELIMINARY; PRT; 401 AA.
ID Q94AE9;
AC Q94AE9;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE AT2G43710/F18019.18.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons: core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Koesema E., Chen H., Cheuk R., Kim C.J., Meyers M.C., Shinn P.,
RA Banh J., Bowser L., Carlincl P., Dale J.M., Gibson H.A.,
RA Goldsmith A.D., Hayashizaki Y., Ishida J., Jiang P.X., Jones T.,
RA Kamuya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J.,
RA Liu S.X., Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,
RA Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
RA Tang C.C., Toriumi M., Yamada K., Yu G., Yu S., Shinozaki K.,
RA Davis R.W., Theologis A., Ecker J.R.;
RT "Arabidopsis cDNA clones."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Meyers M.C., Shinn P., Banh J.,
RA Bowser L., Carlincl P., Chang E., Dale J.M., Goldsmith A.D.,
RA Hayashizaki Y., Ishida J., Jones T., Kamuya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,
RA Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RT "Arabidopsis ORF clones."
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY048233; AAK82496.1; -
DR EMBL: AY094014; AAM16170.1; -
DR InterPro: IPR005067; FA_desat.
DR InterPro: IPR001225; FA_desaturase.
DR Pfam: PF03405; FA_desaturase_2.1.
DR PROSITE: PS00574; FATTY_ACID_DESATUR_2.1.
SQ SEQUENCE 401 AA: 45692 MW: 01F09DD370F4E1D1 CRC64;

Query Match 67.0%; Score 1381.5; DB 10; Length 401;
Best Local Similarity 65.7%; Pred. No. 2.8e-98;
Matches 266; Conservative 61; Mismatches 63; Indels 15; Gaps 6;

QY 1 MALKLNFOCKKNHPAFAKSPPLVPT-RVSSPR-VFMAST---VNSNSWVLDNLKSP----- 51
| | | | | : | | | | | : | | : : | | : : | |
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 1, 2002, 21:18:11 ; Search time 14 Seconds
(without alignments)

1167.262 Million cell updates/sec

Title: US-09-732-597-2

Perfect score: 2062
Sequence: 1 MALKNFOCKKNHPAPAKS.....KKKAHPVFSWIFNRELKI 394

Scoring table: BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1545.5	75.0	385	1 STAD_CORSA	P32063 coriandrum
2	1490	72.3	396	1 STAD_RICCO	P22337 rictinus com
3	1422.5	69.0	411	1 STAD_SOYBN	042807 glycine max
4	1412	68.5	396	1 STAD_CUCSA	P32061 cucumis sat
5	1410.5	68.4	399	1 STAD_SPIOL	P28645 spinacia ol
6	1406	68.2	396	1 STAD_CARTI	P22243 carthamus t
7	1396	67.7	398	1 STAD_BRANA	P29108 brassica na
8	1386.5	67.2	393	1 STAD_SOLCO	041319 solanum com
9	1386.5	67.2	399	1 STAS_BRANA	001771 brassica na
10	1385.5	67.2	393	1 STAD_SOLTV	P46253 solanum tub
11	1385	67.2	390	1 STAD_OLEEU	043593 olea europae
12	1375.5	66.7	397	1 STAD_GOSHI	042770 gossypium h
13	1373	66.6	393	1 STAD_ELAGY	024428 elaeis guin
14	1360	66.0	398	1 STAD_SWICH	001153 simmondsia
15	1352	65.6	396	1 STAD_HELNA	096456 helianthus
16	1310.5	63.6	390	1 STAD_ORYSA	040731 oryza sativ
17	1246	60.4	396	1 STAD_LINUS	P32062 linum usita
18	114.5	5.6	1557	1 DVAL_DICVI	024702 dictyocaulu
19	108	5.2	616	1 K379_METTA	057775 methanococ
20	105.5	5.1	393	1 TRPB_HELPY	092749 hellicobacte
21	102.5	5.0	393	1 Y044_UREPA	P56149 ureaplasma
22	99	4.8	782	1 VATC_METMA	060184 methanosarc
23	98	4.8	360	1 LOX3_PEA	P09918 pisum sativ
24	97.5	4.7	861	1 HEPG_FUSNN	089134 fusobacteri
25	96.5	4.7	607	1 PEPL_HUMAN	060437 homo sapien
26	96.5	4.7	1756	1 TUL3_MOUSE	088413 mus musculu
27	96	4.7	460	1 RA50_SULTO	096875 sulfolobus
28	96	4.7	879	1 NADA_BACSU	094271 bacillus su
29	95	4.6	368	1 MYS3_SCHPO	014157 schizosacch
30	95	4.6	2104	1 CCCL_DROME	094479 drosophila
31	94.5	4.6	524	1 YP94_CAEEL	P41882 caenorhabdi
32	94.5	4.6	1163	1 SAP_HUMAN	P07602 h proactiva
33	93	4.5	524	1	

34	92.5	4.5	574	1 ZDS_NARPS	049901 narcissus p
35	92.5	4.5	1255	1 DIAL_MOUSE	008808 mus musculu
36	92	4.5	526	1 VPS_BTIV1	P33476 bluetongue
37	92	4.5	886	1 RA50_ARCFU	029230 archaeoglob
38	91.5	4.4	426	1 TUB1_CAEEL	009306 caenorhabdi
39	91.5	4.4	1875	1 MLPI_YEAST	002455 saccharomyc
40	91.5	4.4	3685	1 DMD_HUMAN	P11532 homo sapien
41	91.5	4.4	3898	1 POLG_HOVA	P19712 hog cholera
42	91	4.4	552	1 NCAP_TPMV	094540 tupatia para
43	91	4.4	821	1 PPSA_PYROHO	057830 pyrococcus
44	91	4.4	1148	1 YK00_CAEEL	P34305 caenorhabdi
45	91	4.4	2472	1 SPCN_RAT	P16086 rattus norv

ALIGNMENTS

RESULT 1	STAD_CORSA	STANDARD	PRT	385 AA.
ID	STAD_CORSA	STANDARD	PRT	385 AA.
AC	P32063			
DT	01-OCT-1993 (Rel. 27, Created)			
DT	01-OCT-1993 (Rel. 27, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Omega-12 acyl-[acyl-carrier protein] desaturase, chloroplast precursor (EC 1.14.99.6).			
DE	Coriandrum sativum (Coriander).			
OS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids II; Apiales; Apiaceae; Coriandrum.			
OX	NCBI_TaxID=4047;			
RM	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Endosperm;			
RX	MEDLINE=93087491; PubMed=1454797;			
RA	Caheen E.B., Shanklin J., Ohlrogge J.B.;			
RT	"Expression of a coriander desaturase results in petroselinic acid production in transgenic tobacco."			
RL	Proc. Natl. Acad. Sci. U.S.A. 89:11184-11188(1992).			
CC	-1- CATALYTIC ACTIVITY: Stearoyl-[acyl-carrier protein] + AH(2) + O(2)			
CC	-1- Oleoyl-[acyl-carrier protein] + A + 2 H(2)O.			
CC	-1- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.			
CC	-1- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE			
CC	OILS. SPECIFICALLY INVOLVED IN THE SYNTHESIS OF PETROSELINIC ACID.			
CC	-1- SUBUNIT: HOMODIMER (BY SIMILARITY).			
CC	-1- SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PLASTIDS OF			
CC	NONPHOTOSYNTHETIC TISSUES.			
CC	-1- TISSUE SPECIFICITY: FOUND ONLY IN TISSUES WHICH SYNTHESIZE			
CC	PETROSELINIC ACID, SUCH AS DEVELOPING SEEDS.			
CC	-1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.			
CC	-----			
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CC	use by non-profit institutions as long as its content is in no way			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; M93115; AAC63059.1; -			
DR	PIR; A47245; A47245.			
DR	HSSP; P22337; IAFR.			
DR	InterPro; IPR005067; FA_desat.			
DR	InterPro; IPR001225; FA_desaturase.			
DR	RefSeq; PF03405; FA_desaturase_2; 1.			
DR	PROSITE; PS00574; FATTY_ACID_DESATUR_2; 1.			
KW	Oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast;			
KW	Transit peptide.			
FT	CHAIN 1 36 CHLOROPLAST (BY SIMILARITY).			
FT	TRANSIT 37 385 OMEGA-12 ACYL-[ACYL-CARRIER PROTEIN]			
FT	CHAIN 37 385 DESATURASE.			
FT	SEQUENCE 385 AA; 43805 MM; AF79BFB6946EF03 CRC64;			
SO				

Query Match 75.0%: Score 1545.5; DB 1; Length 385;
 Best Local Similarity 73.1%: Pred. No. 3.8e-107;
 Matches 296; Conservative 42; Mismatches 36; Indels 31; Gaps 5;

1 MALKLN-----FOCKKNHPAFAKSPDPYRVSSP-----RVEMASTVNSNSMYLDLKKP 49
 1 MAMLNALMTIQCPRN-----MFTRIAPQAGRVRSKVSMASTLHASPLVFDKIK 51
 50 SPPLQVTHSPPOKLEIFKSLDDMARNNVLIHLKSVESKMPQDYLPPDVSDFEEQVR 109
 52 AG-----RPEVDELFSNLEGARNDIIVHLKSVESKMPQDYLPPDVSDFEEQVR 102
 110 ELERAKELPDYFVVLVGDMTTEALPTVMSLNKCDGKIDETGAESPAMAMWTRAMTA 169
 103 EKREKADIPDEYFVVLVGDMTTEALPTVMSLNKCDGKIDETGAOPTSMATWTRAMTA 162
 170 EENRHGDLNKKYLYLSGRVDMRKTEKTIQYLYLGSGMDIKSENSPYLGFITYTSFORATFI 229
 163 EENRHGDLNKKYLYLSGRVDMRKTEKTIQYLYLGSGMDIKSENSPYLGFITYTSFORATFI 222
 230 SHANTAKLAQHGDGDKLHIGGSIASDEKRNATATYKIEKLAIDPDTTVAIFADMMRK 289
 223 SHANTAKLAQHGDGDKLHIGGSIASDEKRNATATYKIEKLAIDPDTTVAIFADMMRK 282
 290 KITMPAHMLYDGSDELLFHFHTAVAGRVXYXSALDYCDLLEFLVDKMNVERLGLSDEGR 349
 283 KIOMPAHMLYDGSDELLFHFHTAVAGRVXYXSALDYCDLLEFLVDKMNVERLGLSDEGR 342
 350 KAOEYVCELGPKTRVEEYVQGEKKKAHPYSEFSWIFNRELKI 394
 343 KAOEYVCELGPKTRVEEYVQGEKKKAHPYSEFSWIFNRELKI 385

RESULT 2
 STD_RICCO STANDARD; PRT; 396 AA.
 ID STD_RICCO
 AC P22337;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE ACYL-[acyl-carrier protein] desaturase, chloroplast precursor
 (EC 1.14.99.6) (Stearoyl-ACP desaturase) (Delta(9) stearoyl-acyl
 carrier protein desaturase).
 OS Ricinus communis (castor bean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Malpighiales; Euphorbiaceae; Ricinus.
 NC NCBI_TaxID=3988;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91172837; PubMed=2006187;
 RA Shanklin J., Somerville C.R.;
 RT "stearyl-acyl-carrier-protein desaturase from higher plants is
 structurally unrelated to the animal and fungal homologs.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:2510-2514(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX TISSUE-Endosperm;
 RA Knutzen D.S., Scherer D.E., Schreckengost W.E.;
 RT "Nucleotide sequence of a complementary DNA clone encoding stearyl-
 acyl carrier protein desaturase from castor bean, Ricinus communis.";
 RL Plant Physiol. 96:344-345(1991).
 RN [3]
 RX X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
 RA MEDLINE=97015109; PubMed=8861937;
 RA Lindqvist Y., Huang W., Schneider G., Shanklin J.;
 RT "Crystal structure of delta9 stearyl-acyl carrier protein desaturase
 from castor seed and its relationship to other di-iron proteins.";
 RL EMBL J. 15:4081-4092(1996).
 CC -I- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A
 CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL
 CHAIN.

CC -I- CATALYTIC ACTIVITY: Stearoyl-[acyl-carrier protein] + AH(2) + O(2)
 CC -I- OLEOYL-[acyl-carrier protein] + A + 2 H(2)O.
 CC -I- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.
 CC -I- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY
 CC ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE
 CC OILS.
 CC -I- SUBUNIT: HOMODIMER.
 CC -I- SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PLASTIDS OF
 CC NONPHOTOSYNTHETIC TISSUES.
 CC -I- TISSUE SPECIFICITY: HIGHER LEVELS IN DEVELOPING SEEDS THAN IN LEAF
 CC AND ROOT TISSUES.
 CC -I- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
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 CC
 DR EMBL: M59857; AAA74692.1; ALT_INIT.
 DR EMBL: X56508; CAA39859.1; .
 DR PIR: S16463; OHCSAD.
 DR PIR: A39170; A39170.
 DR PDB: 1AER; 15-MAY-97.
 DR InterPro: IPR005067; FA_desat.
 DR InterPro: IPR001225; FA_desaturase.
 DR Pfam: PF03405; FA_desaturase.2; 1.
 DR PROSITE: PS00574; FATTY ACID DESATURASE 2; 1.
 DR Oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast;
 KW Transmembrane; 3D-structure.
 FT TRANSIT 1
 FT CHAIN 34
 FT SEQUENCE 396 AA; 45371 MW; E50d472596392AE CRC64;
 SO

Query Match 72.3%: Score 1490; DB 1; Length 396;
 Best Local Similarity 71.1%: Pred. No. 5e-103;
 Matches 286; Conservative 50; Mismatches 52; Indels 14; Gaps 5;

1 MALKLN-FOCKKNHPAFAKSPDPYRVSSPVRVEMASTVNSNSMYLDLKKP-----PN 53
 1 MALKLNPLSOTQKLPSPALPMASTR--SPKFWASTLKSGSKVEMLKPEMPREYH 58
 54 LQVTHSPPOKLEIFKSLDDMARNNVLIHLKSVESKMPQDYLPPDVSDFEEQVRELRE 113
 59 VQVTHSPPOKLEIFKSLDDMARNNVLIHLKSVESKMPQDYLPPDVSDFEEQVRELRE 118
 114 RAKEIPDDYFVVLVGDMTTEALPTVMSLNKCDGKIDETGAESPAMAMWTRAMTAENR 173
 119 RAKEIPDDYFVVLVGDMTTEALPTVMSLNKCDGKIDETGAESPAMAMWTRAMTAENR 178
 174 HGDLNKKYLYLSGRVDMRKTEKTIQYLYLGSGMDIKSENSPYLGFITYTSFORATFI 233
 179 HGDLNKKYLYLSGRVDMRKTEKTIQYLYLGSGMDIKSENSPYLGFITYTSFORATFI 238
 234 TAKLAQHGDGDKLHIGGSIASDEKRNATATYKIEKLAIDPDTTVAIFADMMRKKTIM 293
 239 TAKLAQHGDGDKLHIGGSIASDEKRNATATYKIEKLAIDPDTTVAIFADMMRKKTIM 298
 294 PAHLMYDGSDELLFHFHTAVAGRVXYXSALDYCDLLEFLVDKMNVERLGLSDEGRKAOE 353
 299 PAHLMYDGSDELLFHFHTAVAGRVXYXSALDYCDLLEFLVDKMNVERLGLSDEGRKAOE 358
 354 YVCELGPKTRVEEYVQGEKKKAHP--VSEFSWIFNRELKI 394
 359 YVCELGPKTRVEEYVQGEKKKAHP--VSEFSWIFNRELKI 396

RESULT 3
 STD_SOYBN STANDARD; PRT; 411 AA.
 ID STD_SOYBN
 AC Q42807;


```

DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Acyl-1-lacyl-carrier protein] desaturase, chloroplast precursor
DE (EC 1.14.99.6) (Stearoyl-ACP desaturase).
GN ACPLD.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_Taxid=3847;
RN [1]
RP SEQUENCE FROM N.A.
RA Chen L., Moon Y., Shanklin J., Nikolau B.J., Atherton A.G.:
RT "Cloning and sequence of a cDNA encoding stearoyl-acyl carrier
RT protein desaturase from Glycine max.";
RL (In) Plant Gene Register PGR95-105.
CC -1- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A
CC CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL
CC CHAIN.
CC -1- CATALYTIC ACTIVITY: Stearoyl-[acyl-carrier protein] + AH(2) + O(2)
CC = oleoyl-[acyl-carrier protein] + A + 2 H(2)O.
CC -1- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.
CC -1- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY
CC ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE
CC OILS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PLASTIDS OF
CC NONPHOTOSYNTHETIC TISSUES (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
CC -----
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CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L34346; AAA92462.1; -.
DR HSSP; P22337; IAFR.
DR InterPro; IPR005067; FA_desat.
DR InterPro; IPR001225; FA_desaturase.
DR Pfam; PF03405; FA_desaturase_2; 1.
DR PROSITE; PS00574; FATTY_ACID_DESATUR_2; 1.
KW Oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast;
KW Transf. peptide.
FT TRANSIT 1 28 CHLOROPLAST (BY SIMILARITY).
FT CHAIN 29 411 ACYL-[ACYL-CARRIER PROTEIN] DESATURASE.
SQ SEQUENCE 411 AA; 47282 MW; 2727C3EDC8C97BA8 CRC64;
Query Match 69.0%; Score 1422.5; DB 1; Length 411;
Best Local Similarity 67.7%; Pred. No.5.2e-98;
Matches 274; Conservative 46; Mismatches 54; Indels 31; Gaps 4;
QY 1 MALKINFOCKKNHPAAFAKSPLPVTRVS-----SPRVFASVNSNSAVLDNLKSP- 51
Db 1 MALRLN-----PIPTQTSFQPMASLRSPFRMASTLRSSGSKVEVNIKRF 46
QY 52 -----PNIQYTHSMPPQKLETFKSLDDMARNNVLIHLKSVESKQWPODYLPDPSVDGEE 106
Db 47 TPPEVHVQVTHSMPPQKLETFKSLDDMARNNVLIHLKSVESKQWPODYLPDPSVDGEE 106
QY 107 QVRELRERAKETLPDQYFVVLGDMTTEELALPYVMSMLRCOSIKQETGAEPSANAMMTRA 166
Db 107 QVRELRERAKETLPDQYFVVLGDMTTEELALPYVMSMLRCOSIKQETGAEPSANAMMTRA 166
QY 167 WTAENRRHGDLLNKLYLSGRVDMKRIEKTIOYLIGSGMDIKSENSPYLGFIYTSFOERA 226
Db 167 WTAENRRHGDLLNKLYLSGRVDMKRIEKTIOYLIGSGMDIKSENSPYLGFIYTSFOERA 226
QY 227 TFIISANTAKLAQHYGDKNLAHIGSISDEKRAATVATKYVERIAEIDPDTVTYAFADM 285
Db 227 TFIISANTAKLAQHYGDKNLAHIGSISDEKRAATVATKYVERIAEIDPDTVTYAFADM 285

```

Dd	227	TFISGNTARLAKKEGDKIKIAQICMTASDEKREHTATVTKYEKLFESDPDGTWAFADM	286
Oy	287	MRRKTTMPAHMLYDSSDELFRHFKFAVAQRXVVSADYCDILEFLVDKNVERLTGLSD	346
		: : : : : : : : : : : :	
Dd	287	MRRKIAMPALHYLDGRDNLEFDNVSSAQRIGVYTAQYADYLEFLVGMRKVVEDJTLGSG	346
Oy	347	EGRKAQEVCELGPKIRRYVEEKVQCKEAKAEHPVSWSPFNRE	391
		: : : : : : : : : :	
Dd	347	EGRKAQEYICGLPPIRIRLRLEERAQRKVESST--LKFSWITHRE	388
		: . :	
RESULT 4			
STAD_CUCSA	STANDARD;	PRT;	396 AA.
ID	STAD_CUCSA	STANDARD;	PRT; 396 AA.
AC	p32061;		
DT	01-OCT-1993 (Rel. 27, Last sequence update)		
DT	01-OCT-1993 (Rel. 27, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
De	Acyl-[acyl-carrier protein] desaturase, chloroplast precursor		
De	(EC 1.14.99.6) (Stearoyl-ACP desaturase).		
OS	Cucumis sativus (Cucumber);		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;		
OC	eurosid I; Cucurbitales; Cucurbitaceae; Cucumiss.		
OX	NCBI_TaxId=3659;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE-Seedling cotyledon;		
RA	Shanklin J., Mullins C., Somerville C.R.;		
RT	"Sequence of a complementary DNA from Cucumis sativus L. encoding the		
RT	stearoyl-acyl-carrier protein desaturase.";		
RL	Plant Physiol. 97:467-468(1991).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=91172637; PubMed=2006187;		
RA	Shanklin J., Somerville C.;		
RT	"Stearyl-acyl-carrier-protein desaturase from higher plants is		
RT	structurally unrelated to the animal and fungal homologs.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 88:2510-2514(1991).		
CC	-I- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A		
CC	CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL		
CC	CHAIN.		
CC	-I- CATALYTIC ACTIVITY: Stearoyl-[acyl-carrier protein] + AH(2) + O(2)		
CC	= oleoyl-[acyl-carrier protein] + A + 2 H(2)O.		
CC	-I- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.		
CC	-I- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY		
CC	ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE		
CC	OILS.		
CC	-I- SUBUNIT: HOMODIMER (BY SIMILARITY).		
CC	-I- SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PLASTIDS OF		
CC	NONPHOTOSYNTHETIC TISSUES.		
CC	-I- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.		
CC	-----		
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CC	use by non-profit institutions as long as its content is in no way		
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/		
CC	or send an email to license@isb-sib.ch).		
CC	-----		
DR	EMBL; M59858; AAA3130.1; -.		
DR	PIR; B39170; B39170.		
DR	HSSP; P22337; 1A9R.		
DR	InterPro; IPR005067; FA_desat.		
DR	InterPro; IPR001225; FA_desaturase.		
DR	Pfam; PF03405; FA_desaturase_2; 1.		
DR	PROSITE; PS00574; FATTY_ACID_DESATUR_2; 1.		
KW	Oxidoreductase; Fatty acid biosynthesis; NMDP; Chloroplast;		
KW	Transit peptide.		
FT	TRANSIT	1	33
FT	CHAIN	34	396
FT	CONFLICT	114	114
		R -> V (IN REF. 2).	

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FT CONFLICT 290 290 E -> D (IN REF. 2).
SQ SEQUENCE 396 AA; 45583 MW; 2E19E894C106D4C8 CRC64;
Query Match 68.5%; Score 1412; DB 1; Length 396;
Best Local Similarity 66.6%; Pred. No. 2.9e-97;
Matches 271; Conservative 51; Mismatches 61; Indels 24; Gaps 5;

OY 1 MALKINFOCKKNHPAFAKSPLEPVR-----VSSPRVFMASVNSNMYLNLKSP---51
DB 1 MALKE-----HPLTQSQPKLPSPFPMQPLASLRSPKFWMASTLRSTREVTLLKPKFMP 53
OY 52 ----PNIQVTHSMPPCKLEIFKSLDDMARNVLIHLKSVKSNOPQDYLPPVSDGFEEOY 108
DB 54 PREVHVQVTHSMPPCKMEIFKSLDDMAEENLVHLKPERKQWQPODPLPDSAFEGEHOY 113
OY 109 RELREKAKEIPDDYFVVLVGMDETEALPTYSMLNRCIDKDETGAPESAMAMTRAWT 168
DB 114 RELREKAKEIPDDYFVVLVGMDETEALPTYSMLNRCIDKDETGAPESAMAMTRAWT 173
OY 169 AEENRHGDLNLKXYLYLGRVDMRKIEKTIQYLLIGSGMDIKSENSPYLGIYTSFOERATF 228
DB 174 AEENRHGDLNLKXYLYLGRVDMRKIEKTIQYLLIGSGMDIKSENSPYLGIYTSFOERATF 233
OY 229 ISHANTAKLAOHGDKNLAIIGSISASDEKRRHATYATKIYEKLAIEDPDYVIAFADMMR 288
DB 234 ISHANTAKLAHKEGDIKLAQICGTTADEKRRHETATKIYEKLEFIDPEGVIAFEEMR 293
OY 289 KRTMPAHMLMYGSDDELFEKFTTAVARVYVSALDYCDILEFLVDKMWNERLTGLSDEG 348
DB 294 KRTMPAHMLMYGSDDELFEKFTTAVARVYVSALDYCDILEFLVDKMWNERLTGLSDEG 353
OY 349 RRAOEYVCELGPKIRVVEKVGKKEKKKAHEP-VSFSWTFNRELKI 394
DB 354 OKADYVCSLPPRIRLEER--AREKAKAP-SMPSWTFIDROVKL 396

RESULT 5
STAD_SPTOL
ID STAD_SPTOL STANDARD; PRT; 399 AA.
AC P28645;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Acyl-[acyl-carrier protein] desaturase, chloroplast precursor
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllales; Chenopodiaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Biotollea; TISSUE=Colyledon;
RX MEDLINE=92329733; PubMed=1627785;
RA Beppu T., Nishida I., Matsuo T., Murata N.;
RT "Nucleotide sequence of a cDNA clone encoding a precursor to
stearyl-[acyl-carrier-protein] desaturase from spinach, Spinacia
oleracea."
RT Plant Mol. Biol. 19:711-713(1992).
RL -1- FUNCTION: CONVERTS STEARYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A
CC C15 DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL
CC CHAIN.
CC -1- CATALYTIC ACTIVITY: Stearoyl-[acyl-carrier protein] + AH(2) + O(2)
CC = oleoyl-[acyl-carrier protein] + A + 2 H(2)O.
CC -1- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.
CC -1- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY
CC ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE
CC OILS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PLASTIDS OF
CC NONPHOTOSYNTHETIC TISSUES.
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.

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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X62898; CAA44687.1; -.
CC PIR: S22480; OHSPAD.
CC DR HSSP: P22337; IAFR.
CC DR InterPro: IPR005067; FA_desat.
CC DR InterPro: IPR001225; FA_desaturase.
CC DR Pfam: PF03405; FA_desaturase-2; 1.
CC DR PROSITE, PS00574; FATTY-ACID-DESATUR-2; 1.
CC KW Oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast;
CC TRANSIT 1
CC TRANSIT 35 CHLOROPLAST.
CC FT CHAIN 36 399 ACYL-[ACYL-CARRIER PROTEIN] DESATURASE.
CC SQ SEQUENCE 399 AA; 45663 MW; 59B5E0609EA7CCC CRC64;

Query Match 68.4%; Score 1410.5; DB 1; Length 399;
Best Local Similarity 67.2%; Pred. No. 3.8e-97;
Matches 273; Conservative 59; Mismatches 55; Indels 19; Gaps 8;

OY 1 MALKIN-----FOCKKNHPAFAKSPLEPVRVSSPRVFMASVNSN-MVLDNLK---SP 51
DB 1 MALNLNPTVSTPFQCR--LPFSFSPROTFSRR--SPKFFMASTLSSSPKEASTLKKPSP 56
OY 52 P---NLOVTHSMPPCKLEIFKSLDDMARNVLIHLKSVKSNOPQDYLPPVSDGFEEOY 108
DB 57 PREVHVQVTHSMPPCKMEIFKSLDDMAEENLVHLKPERKQWQPODPLPDSAFEFEHOY 116
OY 109 RELREKAKEIPDDYFVVLVGMDETEALPTYSMLNRCIDKDETGAPESAMAMTRAWT 168
DB 117 RELREKAKEIPDDYFVVLVGMDETEALPTYSMLNRCIDKDETGAPESAMAMTRAWT 176
OY 169 AEENRHGDLNLKXYLYLGRVDMRKIEKTIQYLLIGSGMDIKSENSPYLGIYTSFOERATF 228
DB 177 AEENRHGDLNLKXYLYLGRVDMRKIEKTIQYLLIGSGMDIKSENSPYLGIYTSFOERATF 236
OY 229 ISHANTAKLAOHGDKNLAIIGSISASDEKRRHATYATKIYEKLAIEDPDYVIAFADMMR 288
DB 237 VSHGNSARLAHEHGLKMAQICGTTASDEKRRHETATKIYEKLEFIDPDATVLAADMMK 296
OY 289 KRTMPAHMLMYGSDDELFEKFTTAVARVYVSALDYCDILEFLVDKMWNERLTGLSDEG 348
DB 297 KRTMPAHMLMYGSDDELFEKFTTAVARVYVSALDYCDILEFLVDKMWNERLTGLSDEG 356
OY 349 RRAOEYVCELGPKIRVVEKVGKKEKKKAHEPVSFSWTFNRELKI 394
DB 357 OKADYVCSLPPRIRLEER--AREKAKAP-SMPSWTFIDROVKL 399

RESULT 6
STAD_CARTI
ID STAD_CARTI STANDARD; PRT; 396 AA.
AC P22243;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Acyl-[acyl-carrier protein] desaturase, chloroplast precursor
OS Carthamus tinctorius (Safflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; eusterids II; Asterales; Asteraceae; Cardueae; Carthamus.
OX NCBI_TaxID=4222;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Seed;
RX MEDLINE=91172850; PubMed=2006194;
RA Thompson G.A., Scherer D.E., Foxall-Van Aken S., Kenny J.W.,

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RA Young H.L., Shintani D.K., Kridel J.C., Knauf V.C.;
 RT "Primary structures of the precursor and mature forms of
 RT stearoyl-acyl carrier protein desaturase from safflower embryos and
 RT requirement of ferredoxin for enzyme activity.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:2578-2582(1991).
 CC -1- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A
 CC CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL
 CC CHAIN.
 CC -1- CATALYTIC ACTIVITY: Stearoyl-[acyl-carrier protein] + AH(2) + O(2)
 CC = oleoyl-[acyl-carrier protein] + A + 2 H(2)O.
 CC -1- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.
 CC -1- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY
 CC ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE
 CC OILS.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PLASTIDS OF
 CC NONPHOTOSYNTHETIC TISSUES.
 CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
 CC -----
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 CC -----
 CC EMBL: M61109; AAA3021.1; -
 CC DR PIR: A39173; A39173.
 CC DR HSSP: P22337; IAFR.
 CC DR InterPro: IPR005067; FA_desat.
 CC DR InterPro: IPR001225; FA_desaturase.
 CC DR Pfam: PF03405; FA_desaturase_2; 1.
 CC DR PROSITE: PS00574; FATTY_ACID_DESATUR_2; 1.
 CC DR Oxidoreductase: Fatty acid biosynthesis; NADP; Chloroplast;
 CC KW Transist peptide.
 CC TRANSIT 1 33 CHLOROPLAST
 CC FT CHAIN 1 396 ACYL-[ACYL-CARRIER PROTEIN] DESATURASE.
 CC FT MOD_RES 34 34 BLOCKED (PARTIAL).
 CC SQ SEQUENCE 396 AA; 45054 MW; 7B14529889D39087 CRC64;

Query Match 68.2%; Score 1406; DB 1; Length 396;
 Best Local Similarity 67.1%; Pred. No. 8.2e-97;
 Matches 271; Conservative 54; Mismatches 61; Indels 18; Gaps 5;

1 MALKL---NFQCKKNHPAFAKSPLEPTRVSSPRVFMASTVNSMVLNLSKSP----- 51
 1 MALRLTPVTLQSEKRRSEFFPKK---ANLRSPKFMASLTGSTRKVDNAKKPPPPRE 56
 52 PVLQVTHSNPQKLEIFKSLDWMARNVLIHLKSVKSNQPODYLPDPVSDGFEQVREL 111
 57 VHVQVTHSNPQKLEIFKSLDWMARNVLIHLKSVKSNQPODYLPDPVSDGFEQVREL 116
 112 RRAREIPDDYVNVVGVDMTEALPTVMSMLNRGCIIDENGAESNAAMVRAATAAE 171
 117 RRAREIPDDYVNVVGVDMTEALPTVMSMLNRGCIIDENGAESNAAMVRAATAAE 175
 172 NRHGDLNKLKLYLISGRVDMARKIEKTIQVYLGSGMDIKSENSPYLIGTYISFOERATFIS 231
 177 NRHGDLNKLKLYLISGRVDMARKIEKTIQVYLGSGMDIKSENSPYLIGTYISFOERATFIS 236
 232 ANTKALAOHYGCKNLALHICGSIASDEKRNATYATKIVKELAEIDPTVYIAEADMRRKKI 291
 237 GNTAHAKDHGCVKLAOLICGTIASDEKRNATYATKIVKELAEIDPTVYIAEADMRRKKI 296
 292 TMPAHLMVDSDELLEFKHTTAAVAAORXYVSAIDYCDILEFLVDKMNVEVLGTGSDGKRA 351
 297 SMPAHLMVDSDELLEFKHTTAAVAAORXYVSAIDYCDILEFLVDKMNVEVLGTGSDGKRA 356
 352 QEVYCELGPRIKRVKEKVGKKKKAEHP-VSFSWIFNRELKI 394
 357 QDVYVGLPRIRIRLEERAGRAK---EGPVVPEFSWIFNROYKL 396

RESULT 7
 STAD_BRANA STANDARD; PRT; 398 AA.
 ID STAD_BRANA
 AC P29108;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Acyl-[acyl-carrier protein] desaturase, chloroplast precursor
 DE (EC 1.14.99.6) (Stearoyl-ACP desaturase).
 OS Brassica napus (Rape).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Brassica.
 OX NCBI_TaxID=3708;
 RX MEDLINE=92212861; PubMed=1557366;
 RX Knutzon D.S., Thompson G.A., Radke S.E., Johnson W.B., Knauf V.C.,
 RA Kridel J.C.;
 RA "Modification of Brassica seed oil by antisense expression of a
 RT stearoyl-acyl carrier protein desaturase gene.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2624-2628(1992).
 RL [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=CV, Jet neuf; TISSUE=leaf;
 RX MEDLINE=97260965; PubMed=9107041;
 RA Piffanelli P., Ross J.H., Murphy D.J.;
 RT "Intra- and extracellular lipid composition and associated gene
 RT expression patterns during pollen development in Brassica napus.";
 RL Plant J. 11:549-562(1997).
 CC -1- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A
 CC CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL
 CC CHAIN.
 CC -1- CATALYTIC ACTIVITY: Stearoyl-[acyl-carrier protein] + AH(2) + O(2)
 CC = oleoyl-[acyl-carrier protein] + A + 2 H(2)O.
 CC -1- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.
 CC -1- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY
 CC ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE
 CC OILS.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PLASTIDS OF
 CC NONPHOTOSYNTHETIC TISSUES.
 CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
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 CC -----
 CC EMBL: X60978; CAA43294.1; -
 CC DR EMBL: X97325; CAA65990.1; -
 CC DR PIR: S23351; S23351.
 CC DR HSSP: P22337; IAFR.
 CC DR InterPro: IPR005067; FA_desat.
 CC DR InterPro: IPR001225; FA_desaturase.
 CC DR Pfam: PF03405; FA_desaturase_2; 1.
 CC DR PROSITE: PS00574; FATTY_ACID_DESATUR_2; 1.
 CC DR Oxidoreductase: Fatty acid biosynthesis; NADP; Chloroplast;
 CC KW Transist peptide.
 CC TRANSIT 1 34 CHLOROPLAST (BY SIMILARITY).
 CC FT CHAIN 1 398 ACYL-[ACYL-CARRIER PROTEIN] DESATURASE.
 CC SQ SEQUENCE 398 AA; 45347 MW; 9DD689FCF841C5F5 CRC64;

Query Match 67.7%; Score 1396; DB 1; Length 398;
 Best Local Similarity 66.9%; Pred. No. 4.5e-96;
 Matches 269; Conservative 55; Mismatches 66; Indels 12; Gaps 4;

1 MALKLNFQCKKNHPAFAKSPLEPTRVSSPRVFMASTVNSMVLNLSKSP-----P 52

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Db      1  MALKLNPLASQPYNFBSS -ARPTSTFRRSKFLCLCLASSSPALSSKEVESLKKPFPPPREKVEV  59
OY      53  NLOVTHSMPEPOKLEIFKSLTDDMARNNVLHLKSVKSWQPODYLDPDVSDFGEQVRELR  112
Db      60  HVQYJHSMPPQKLEIFKSMEDMAEQNLTLQKRYEKSWSQODELDPDPASGEFDQVRELR  119
OY      113  ERAKEIPDDYFVYVJGSMITHEALPTMYMSLNLNCDGKIDETGAEPESAMAMWTAPMAAEEN  172
Db      120  ERARELPDDYFVYVJGSMITHEALPTQMLNMLDQVREDTGAISPMSALWTAPMAAEEN  179
OY      173  RHGDLNKKYLLSGRVDMRKIEKTIQYLLIGSGMDIKSENSPYGLFYTSFOERATPISHA  232
Db      180  RHGDLNKKYLLSGRVDMRKIEKTIQYLLIGSGMDPRTENNPPYLGFIYTSFOERATPISHG  239
OY      233  NTAKLAQHYGDKNLAHICGSJASDEKHNHATYKTVKLAIEIDPDTVIAFADMMRKITP  292
Db      240  NTARAKDHGDLKLAOICGTLAADEKHNHTYKTVKLELEIDPDGVIAFADMMRKITS  299
OY      293  MPAHLMYGSDELLFKHPTAVAQGVXYXVSAJDYCDLEFLVDKWNVERLTGLSDEGKAAQ  352
Db      300  MPAHLMYGRBESLFDNRSVVAQRIGVYATADYADILEFLVGWRKIESTLGLSGEKNKAQ  359
OY      353  EYVCELGPKIRIRVEKEVQVQGEKKKKKAHPVSPFSMLINPREKI  394
Db      360  EYLCGLTPIRIRLDERAARAKKGD--KVPSSMTHDEVOVL  398

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CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Chloroplast (Probable).
CC -1- TISSUE SPECIFICITY: DEVELOPING SEED.
CC -1- DEVELOPMENTAL STAGE: INDUCED BY 25 DAYS AFTER ANTHESIS (DAA),
CC PEAKING AT 45 DAA BUT DECREASING CONSIDERABLY THEREAFTER.
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
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CC -----
DR EMBL: X63364; CA44964.1; -.
DR PIR: S24995; S24995.
DR HSSP: P22337; IAFR.
DR InterPro: IPR005067; FA_desat.
DR InterPro: IPR001225; FA_desaturase.
DR Pfam: PF03405; FA_desaturase_2; 1.
DR PROSITE: PS00574; FATTY_ACID_DESATUR_2; 1.
KW Oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast;
KM Transit peptide.
FT TRANSIT 1 34 CHLOROPLAST (BY SIMILARITY).
FT CHAIN 35 399 ACYL-[ACYL-CARRIER PROTEIN] DESATURASE.
FT SEQUENCE 399 AA; 45358 MW; 8537254C13D9AF80 CRC64;
SQ
Query Match 67.2%; Score 1386.5; DB 1; Length 399;
Best Local Similarity 65.8%; Pred. No. 2.3e-95;
Matches 265; Conservative 59; Mismatches 66; Indels 13; Gaps 4;
QY 1 MALKLNFOCKKHHPAFAKSPLYTRVSSPRVFMASTVNS--NSMVLNLIKSP----- 51
DB 1 MALKFNPLVSGPYKLASSARP-PVSTFRSPFELCLASSSSPALSKVEESLKKPTPPRE 59
QY 52 PNLQVTHSMPPQKLEIFKSLDDMARNNVLIHLKSVKSMQPODYLDPVSDGFEQVREL 111
DB 60 VHLQVTHSMPPQKLEIFKSMEDRAEQNLPLHLKDKVKSMDQDFLPDPAISDGFEDQVEL 119
QY 112 RERAKEIPDDVFNVLVGMITEEALPTYSMLNRCDGIKDENGAESPAMAMTRAMTAE 171
DB 120 RERARELPDDVFNVLVGMITEEALPTYTMLNTLDGRDETGAESPMAVTRAMTAE 179
QY 172 NRHGDLLNKLYLSGRVDMRKTEKTIQYLLIGSGMDIKSENSPYLGIYTSFQERATFISH 231
DB 180 NRHGDLLNKLYLSGRVDMRKTEKTIQYLLIGSGMDPRTEENNPYLGFIYTSFQERATFVSH 239
QY 232 ANTKLAOHYGDKNLAHTICGSIASDEKRRHATYTKIVEKLAIEDPTTVIAFADMRKKI 291
DB 240 GNTPARQAKHEHDLKLAQICGTIADEKRRHETAYTKIVEKLEIDPDGTVAFAADMRRKI 299
QY 292 TMPRLHWYDGSDELLEKFTTAVAORVXYVYALDYCDLLEFLVDKMNVRRLTGLSGEGRA 351
DB 300 SMPRLHWYDGSDDNLDNFDFSSVAORLGYTTAKVDADLLEFLAGRRIRISLTGLSGEGRA 359
QY 352 QEYVCELGPKIRRVEEKVQGEKKRKAHPVSFSWIFNRELKI 394
DB 360 QEYVCELGPKIRRLRDERAQRARAKGP---KIPFSWIHREVOQL 399
RESULT 10
STAD_SOLITU STANDARD: PRT; 393 AA.
AC P46253;
DT 01-NOV-1995 (Rel. 32, Last Created)
DT 15-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Acyl-[acyl-carrier protein] desaturase, chloroplast precursor
DE (RC 1.14.99.6) (Stearoyl-ACP desaturase).
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_Taxid=4113;
RN [1]
RP SEQUENCE FROM N.A.
RA Taylor M.A., Smith S.B., Davies H.V., Burch L.R.;
RL Submitted (XXY1992) to the EMBL/GenBank/DDBJ databases.
CC -1- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A
CC CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL
CC CHAIN.
CC -1- CATALYTIC ACTIVITY: Stearoyl-[acyl-carrier protein] + AH(2) + O(2)
CC = oleoyl-[acyl-carrier protein] + A + 2 H(2)O.
CC -1- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.
CC -1- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY
CC ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE
CC OILS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PLASTIDS OF
CC NONPHOTOSYNTHETIC TISSUES (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
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CC -----
DR EMBL: M91238; AAA3839.1; -.
DR HSSP: P22337; IAFR.
DR InterPro: IPR005067; FA_desat.
DR InterPro: IPR001225; FA_desaturase.
DR Pfam: PF03405; FA_desaturase_2; 1.
DR PROSITE: PS00574; FATTY_ACID_DESATUR_2; 1.
KW Oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast;
KM Transit peptide.
FT TRANSIT 1 30 CHLOROPLAST (BY SIMILARITY).
FT CHAIN 31 393 ACYL-[ACYL-CARRIER PROTEIN] DESATURASE.
FT SEQUENCE 393 AA; 44538 MW; 3FBCC282D57CA7FF CRC64;
SQ
Query Match 67.2%; Score 1385.5; DB 1; Length 393;
Best Local Similarity 64.5%; Pred. No. 2.7e-95;
Matches 258; Conservative 62; Mismatches 67; Indels 13; Gaps 4;
QY 1 MALKLNFOCKKHHPAFAKSPLYTRVSSPRVFMASTVNSMVLNLIKSP---SP---NL 54
DB 1 MALNTNGVSLKSHKML-----PEPCSSARSERFVMASTIRPSVEGVSVKATFPREVHY 56
QY 55 QVTHSMPPQKLEIFKSLDDMARNNVLIHLKSVKSMQPODYLDPVSDGFEQVRELRLER 114
DB 57 QVTHSMPPREKIEVFSLRMAAQNLIHLKPYEKCQMPDFLPDPAISEGFEQVKELRLER 116
QY 115 AKETIPDDVFNVLVGMITEEALPTYSMLNRCDGIKDENGAESPAMAMTRAMTAEENH 174
DB 117 KEIIPDDVFNVLVGMITEEALPTYTMLNTLDGVDEGATVPAWTRAMTAEENH 176
QY 175 GDLNKKYLLLSGRVDMRKTEKTIQYLLIGSGMDIKSENSPYLGIYTSFQERATFISHANT 234
DB 177 GDLNKKYLLLSGRVDMRKTEKTIQYLLIGSGMDPRTEENNPYLGFIYTSFQERATFVSHGNT 236
QY 235 AKLAOHYGDKNLAHTICGSIASDEKRRHATYTKIVEKLAIEDPTTVIAFADMRKKITMP 294
DB 237 ARLAKHEGDMKLAQICGSIASDEKRRHETAYTKIVEKLEIDPDGTVAFAADMRRKISMP 296
QY 295 AHLMTYDGSDELLEKFTTAVAORVXYVYALDYCDLLEFLVDKMNVRRLTGLSGEGRAQCY 354
DB 297 AHLMTYDGRDNLFEHPSAAVORLGYTTAKVDADLLEFLHGRMVEKLTGLSGEGRAQDY 356
QY 355 VCELGPKIRRVEEKVQGEKKRKAHPVSFSWIFNRELKI 394
DB 357 VCGIAPRIKLEBRQARAKHNKS---VPSFMTFGKEITL 393
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RESULT 11

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STAD_OLEU      STANDARD:      PRT:      390 AA.
ID   STAD_OLEU      04593;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Acyl-[acyl-carrier protein] desaturase, chloroplast precursor
    (EC 1.14.99.6) (Stearoyl-ACP desaturase).
OS   Olea europaea (Common olive).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC   Asteridae; euasterids I; Lamiales; Oleaceae; Olea.
OX   NCBI_TaxID=4146;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Leccino; TISSUE=mesocarp;
RA   Baldoni L., Georgi L., Abbott A.G.;
RT   "Nucleotide sequence of a cDNA clone from Olea europaea encoding a
    stearyl-acyl carrier protein desaturase.";
RL   (In) Plant Gene Register PGR96-052.
CC   -1- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A
    CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL
    CHAIN.
CC   -1- CATALYTIC ACTIVITY: Stearoyl-[acyl-carrier protein] + AH(2) + O(2)
    = oleoyl-[acyl-carrier protein] + A + 2 H(2)O.
CC   -1- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.
CC   -1- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY
    ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE
    OILS.
CC   -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC   -1- SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PLASTIDS OF
    NONPHOTOSYNTHETIC TISSUES (BY SIMILARITY).
CC   -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
CC   -----
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CC   -----
DR   EMBL: U58141; AAB67840.1; -.
DR   HSSP: P22337; IAFR.
DR   InterPro: IPR005067; FA_desat.
DR   InterPro: IPR001225; FA_desaturase.
DR   Pfam: PF03405; FA_desaturase_2; 1.
DR   PROSITE: PS00574; FATTY_ACID_DESATUR_2; 1.
KW   oxidoreductase; fatty acid biosynthesis; NADP; chloroplast;
    trans.
FT   TRANSIT      1      27      CHLOROPLAST (BY SIMILARITY).
FT   CHAIN        28      390      ACYL-[ACYL-CARRIER PROTEIN] DESATURASE.
SQ   SEQUENCE      390 AA; 44596 MW; 39090EA32B7AC2E3 CRC64;
Query Match      67.2%; Score 1385; DB 1; Length 390;
Best Local Similarity 66.3%; Pred. No. 2.9e-95;
Matches 266; Conservative 55; Mismatches 62; Indels 18; Gaps 5;
1  MALKLNFOCKNHPAFAKSP-LPTRVSSPRVMASTVNSNAYLDNLKSP-----PN 53
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db  1  MALKL-----CFPP-----KMPSPFARIRSRHVRVMASTIHSPSMGVKVFPPREVV 52
QY  54  LQVTHSMPPQRLKLFKSLDDARNNNVLIHLKSVKSPQDYLPPVSDGEFEQVRELRE 113
   :|||: | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db  53  VQVTHSLAPKRELFNSINNNAOENILVLKLDVDCWQSPDLPPSASGPFQVMELEK 112
QY  114  RAKELPPDYFVVLVDMTTEALPTVMSLNRCDIGIKDETGAPEPSAMWMTAAMTAENR 173
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db  113  RCKELPPDYFVVLVDMTTEALPTVYQTMNLGVRDETGSLLPMAIWTAMTAENR 172
QY  174  HGDLNKLVLTLGSRVDMKRIEKTIOYLIGSCMDIKSENSPYLGFITYSFQERATFISHAN 233

```

RESULT 12

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STAD_GOSHI      STANDARD:      PRT:      397 AA.
ID   STAD_GOSHI      042770;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Acyl-[acyl-carrier protein] desaturase, chloroplast precursor
    (EC 1.14.99.6) (Stearoyl-ACP desaturase).
OS   Gossypium hirsutum (Upland cotton).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Malvales; Malvaceae; Gossypium.
OX   NCBI_TaxID=3635;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Deltafine 16;
RA   Liu Q., Singh S., Sharp P., Green A., Marshall D.R.;
RT   "Nucleotide sequence of a cDNA from Gossypium hirsutum encoding a
    stearyl-acyl carrier protein desaturase.";
RL   (In) Plant Gene Register PGR96-018.
CC   -1- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A
    CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL
    CHAIN.
CC   -1- CATALYTIC ACTIVITY: Stearoyl-[acyl-carrier protein] + AH(2) + O(2)
    = oleoyl-[acyl-carrier protein] + A + 2 H(2)O.
CC   -1- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.
CC   -1- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY
    ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE
    OILS.
CC   -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC   -1- SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PLASTIDS OF
    NONPHOTOSYNTHETIC TISSUES (BY SIMILARITY).
CC   -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
CC   -----
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
    between the Swiss Institute of Bioinformatics and the EMBL outstation -
    the European Bioinformatics Institute. There are no restrictions on its
    use by non-profit institutions as long as its content is in no way
    modified and this statement is not removed. Usage by and for commercial
    entities requires a license agreement (See http://www.isb-sib.ch/announce/
    or send an email to license@isb-sib.ch).
CC   -----
DR   EMBL: X95988; CAA65232.1; -.
DR   HSSP: P22337; IAFR.
DR   InterPro: IPR005067; FA_desat.
DR   InterPro: IPR001225; FA_desaturase.
DR   Pfam: PF03405; FA_desaturase_2; 1.
DR   PROSITE: PS00574; FATTY_ACID_DESATUR_2; 1.
KW   oxidoreductase; fatty acid biosynthesis; NADP; chloroplast;
    trans.
FT   TRANSIT      1      33      CHLOROPLAST (BY SIMILARITY).
FT   CHAIN        34      397      ACYL-[ACYL-CARRIER PROTEIN] DESATURASE.
SQ   SEQUENCE      397 AA; 45233 MW; 5FAA220238B2C37A CRC64;
Query Match      66.7%; Score 1375.5; DB 1; Length 397;
Best Local Similarity 67.7%; Pred. No. 1.5e-94;
1  HGDLNKLVLTLGSRVDMKRIEKTIOYLIGSCMDIKSENSPYLGFITYSFQERATFISHAN 232
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db  173  HGDLNKLVLTLGSRVDMKRIEKTIOYLIGSCMDIPRENNPYLGFITYSFQERATFISHGN 232
QY  234  TAKLAOHYGDKNLAHICGSIASDEKRNATATYKIVEKIAEIDPDPTVIAFADMMRKRTM 293
   |||: | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db  233  TARLAKEHGLKLAIOICGIIAIADEKREHETATYKIVEKLEFIDPDGVIALADMRKRVSM 292
QY  294  PAHLMTDGSSELLFKHPTAVAGRVXYSAUDYCDILEFLVDKMNVERLTGIDSGRKAQE 353
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db  293  PAHLMTDGDGDNLFENFSSAOKLGYTTAKDYADILEFLVGRMDIEKTLGSGGRKAQD 352
QY  354  YVCELGPRIKVEEKYQKREKRAKAEHPVSFWIFNRELKI 394
   || | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db  353  YVCTLPPRIKRIEBAQSRVKKASA--TPFSWIFGREINL 390

```


Matches 272; Conservative 41; Mismatches 76; Indels 13; Gaps 6;

OY 1 MALKINFCCKNHP-AAPAKSPLPYTRVSSPRFVMASTVNSMWLDNLK---SPN--- 53
D 1 MALNFNNAISKSKLPKLPALPKATLR--SPKFSMISTPISGSKREKGNLKKPFTPKVEVP 58
OY 54 LQVTHSNPQKLEIFKSLDDMARNNVLHLKSVKSMQPDYLPDPVSGFEQVRELE 113
D 59 VOITHSNMPKHEIFKSLGMAENNLHLKREKQPADLPDPNSGCFHEQVRELE 118
OY 114 RAKEIPDYPFVVLQDMTEALPTYSMLNRCGIDKGTGAPSAMAMWTAMPAEENR 173
D 119 RAKEIPDYPFVVLQDMTEALPTYSMLNRCGIDKGTGAPSAMAMWTAMPAEENR 178
OY 174 HGDLINKLYLSGRVDMRKIEKTIQYLLGSGMDIKSENSPYLGFIYTSFOERATFISHAN 233
D 179 HGDLINKLYLSGRVDMRKIEKTIQYLLGSGMDIKSENSPYLGFIYTSFOERATFISHAN 238
OY 234 TAKLAQHYGDMKLAHICGSIASDEKRNATATYKIEKLAIDPDTVIAFADMMKKITM 293
D 239 TGRLAKEYGDLINLAQICGSIASDEKRNATATYKIEKLAIDPDTVIAFADMMKKITM 298
OY 294 PAHLMYDSDLELFKHTFAVQRYVYALDYCDILEFLVDKMWVERLTGLSDEGRKAOE 353
D 299 PAEFLYDGRDNLDPHYSAVAQRIYVYAKDYVDIVENHVDKMKKELAGLSAEGRKAD 358
OY 354 YVCELGPKIRVVEEKVGKERRKKAHEPV--FSWIFNRELKI 394
D 359 YLCSLPISRIRLEERAQ---EKAGSTPVSPSWIFNREVKL 397

RESULT 13
STAD_ELAVY STANDARD; PRT; 393 AA.

AC 024428;
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE ACYL-[acyl-carrier protein] desaturase, chloroplast precursor
DE (EC 1.14.99.6) (Stearoyl-ACP desaturase).
OS *Elaeis guineensis* var. *tenera* (Oil palm).
OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Arecaeae; Arecoidae;
OC Coccoae; Elaeidinae; Elaeis.
OX NCBI_TaxID=51953;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Mesocarp;
RA Shah F.H., Rashid O.;
RT "Nucleotide sequence of a cDNA clone encoding stearoyl-acyl-carrier-
protein from *Elaeis guineensis* var. *tenera*.";
RL (in) Plant Gene Register PGR96-110.
CC -1- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A
CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL
CHAIN.
CC -1- CATALYTIC ACTIVITY: Stearoyl-[acyl-carrier protein] + AH(2) + O(2)
CC -1- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.
CC -1- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY
ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE
OILS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PLASTIDS OF
NONPHOTOSYNTHETIC TISSUES (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC DR EMBL: U68756; AAB41041.1; ALT_INIT.
DR HSSP: P22337; IAFR.
DR InterPro: IPR005067; FA_desat.
DR InterPro: IPR001225; FA_desaturase.
DR Pfam: PR03405; FA_desaturase_2; 1.
DR PROSITE: PS00574; FATTY_ACID_DESATUR_2; 1.
KW Oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast;
KW Transmembrane protein;
KW TRANSIT 1 31 CHLOROPLAST (BY SIMILARITY).
FT CHAIN 32 393 ACYL-[ACYL-CARRIER PROTEIN] DESATURASE.
SQ SEQUENCE 393 AA; 44857 MW; C6A8788B80D8A0CC CRC64;

Query Match 66.6%; Score 1373; DB 1; Length 393;
Best local similarity 68.0%; Pred. No. 2.2e-94;
Matches 264; Conservative 55; Mismatches 59; Indels 10; Gaps 6;

OY 14 PAAF-AKSPLEPYTR-VSSPRFVMASTVNSMWLDNLK---SPN---NLQVTHSNPQKLE 66
D 9 PEAFLECFSPKKTTRSTRSPRISMASTVSGPSTKVEIPKPKPMPREVHVOYTHSNPQKIE 68
OY 67 IFKSLDMMARNNVLHLKSVKSMQPDYLPDPVSGFEQVRELERAKEIPDYPFVVL 126
D 69 IFKSLDMMARNNVLHLKSVKSMQPDYLPDPVSGFEQVRELERAKEIPDYPFVVL 128
OY 127 VGDMLTEALPTYMSMLNRCGIDKGTGAPSAMAMWTAMPAEENRHGDLNKKYLYLSG 186
D 129 VGDMLTEALPTYMSMLNRCGIDKGTGAPSAMAMWTAMPAEENRHGDLNKKYLYLSG 188
OY 187 RVDMMKIEKTIQYLLGSGMDIKSENSPYLGFIYTSFOERATFISHANTAKLAQHYGDKNL 246
D 189 RVDMMKIEKTIQYLLGSGMDIKSENSPYLGFIYTSFOERATFISHANTAKLAQHYGDKNL 248
OY 247 AHICGSIASDEKRNATATYKIEKLAIDPDTVIAFADMMKKITMPAHLMYDSDLE 306
D 249 AHICGSIASDEKRNATATYKIEKLAIDPDTVIAFADMMKKITMPAHLMYDSDLE 308
OY 307 FKHFTVAQRYVYALDYCDILEFLVDKMWVERLTGLSDEGRKAOEYCELGPKIRVE 366
D 309 FEHFSVAQRYVYALDYCDILEFLVDKMWVERLTGLSDEGRKAOEYCELGPKIRVE 368
OY 367 EKVQGEKKKKAHPRFSNIFNRELKI 394
D 369 ERAQ---ERAKQAPR-IPCSWYIGREVOL 393

RESULT 14
STAD_STMCH STANDARD; PRT; 398 AA.

AC 001753;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE ACYL-[acyl-carrier protein] desaturase, chloroplast precursor
DE (EC 1.14.99.6) (Stearoyl-ACP desaturase).
OS *Simmondsia chinensis* (Jojoba).
OC Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Simmondsiaceae; Simmondsia.
OX NCBI_TaxID=39993;
RN [1]
RP SEQUENCE FROM N.A.
RA Sato A., Becker C.K., Knaut V.C.;
RT "Nucleotide sequence of a complementary DNA clone encoding stearoyl-
acyl carrier protein desaturase from *Simmondsia chinensis*.";
RL Plant Physiol. 99:362-363(1992).
CC -1- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A
CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL
CHAIN.
CC -1- CATALYTIC ACTIVITY: Stearoyl-[acyl-carrier protein] + AH(2) + O(2)
CC -1- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.
CC -1- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY

Search completed: December 1, 2002, 21:20:34
Job time : 16 secs

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DR WPI: 1995-253884/33.
DR N-PSDB: AAQ92889.
XX New omega-12 desaturase from coriander - and DNA encoding it, useful
PT for making transgenic plants able to synthesise petroselinic acid.
XX
XX
PS Claim 4; Columns 18; 25pp; English.
XX
XX A cDNA library prep. from developing seeds of coriander was
CC screened with a probe based on a partial cDNA clone (AAQ92888) of
CC omega-12 desaturase to isolate full-length clone EC201 (AAQ92889).
CC Expression of this cDNA in transgenic tobacco callus resulted in
CC prodn. of petroselinic acid (18:1 omega 12) and omega-12
CC hexadecenoic acid.
XX
XX Sequence 385 AA:
SQ
Query Match 75.0%; Score 1545.5; DB 16; Length 385;
Best Local Similarity 73.1%; Pred. No. 7.3e-140;
Matches 296; Conservative 42; Mismatches 36; Indels 31; Gaps 5;
OY 1 MALKLN----FOCKKNHPAFAKSPLEVRVSSP-----RVFMASTVNSNSMVLNDLTK 49
DB 1 MAMKLNALMTLQCPKRN-----MFTRIAPQAGRVRSKVSMASTLHSLVFDKTK 51
OY 50 SPPNLOVTHSMPPQKLEIFKSLDDMARNNVLHLKSVKSWQPODYLPDPVSDGFEEQVR 109
DB 52 AG-----RPEVDELFSLEGWARDNTLVHLKSVENSWOPODYLPDPTSDAFEEQVK 102
OY 110 ELREAKEIPDDQFVVLVGMITEEALPTYMSMLNRCDDIKDETGAEPSSAMWTRAMTA 169
DB 103 EMERKAKDIPDELFVVLVGMITEEALPTYMSMLNRCDDIKDETGAEPSSAMWTRAMTA 162
OY 170 EENRHGDLNKLKYLISGRVDMRKTEKTOYLIGSGMDIKSENSPYLGFIYTSFOERATFI 229
DB 163 EENRHGDLNKLKYLISGRVDMRKTEKTOYLIGSGMDIKSENSPYLGFIYTSFOERATFI 222
OY 230 SHANTAKLAOHYGDKNIAHIGSISASDERKHAATYKIVEKLAIEDPDTTVIAFADMMRK 289
DB 223 SHANTAKLAOHYGDKNIAHIGSISASDERKHAATYKIVEKLAIEDPDTTVIAFADMMRK 282
OY 290 KIMPAPHAMWDSDELFEKHFHTAQAQRVXYASALDYCDILEFLVDKMWVERLTGLSDEGR 349
DB 283 KIMPAPHAMWDSDELFEKHFHTAQAQRVXYASALDYCDILEFLVDKMWVERLTGLSDEGR 342
OY 350 KAOEYVCELGPKTRVEEKVQGEKKKKAEPSPFSWTFNRRLKI 394
DB 343 KAOEYVCELGPKTRVEEKVQGEKKKKAEPSPFSWTFNRRLKI 385
RESULT 2
AAW44350
ID AAW44350 standard; Protein; 396 AA.
XX
XX AAW44350:
XX
XX 28-MAY-1998 (first entry)
XX
DE Ricinus communis desaturase from clone pCGN3230.
XX
XX Ricinus communis; castor bean; delta-9 desaturase; oilseed;
KM fatty acid saturation.
XX
XX
OS Ricinus communis.
XX
XX US5723595-A.
XX
XX 03-MAR-1998.
XX
XX 06-JUN-1995; 95US-0471791.
XX
XX 16-SEP-1991; 91US-0762762.
XX
XX 16-MAR-1990; 90US-0494106.
PR

PR 13-AUG-1990; 90US-0567373.
PR 14-NOV-1990; 90US-0615784.
PR 14-MAR-1991; 91MO-US01746.
PR 06-JUN-1995; 95US-0471791.
XX
XX (CALT) CALGENE INC.
XX
XX Knaut VC, Thompson GA;
XX
XX
XX WPI: 1998-178544/16.
XX
XX N-PSDB: AAV15252.
XX
XX DNA encoding plant delta-9 desaturase protein - having amino acid
PT sequence of Carthamus tinctorius desaturase, useful for, e.g.
PT producing oil-seeds with modified levels of fatty acid saturation
XX
XX
XX Claim 7; Column 59-60; 87pp; English.
XX
XX
XX The present sequence represents a Ricinus communis desaturase from
CC clone pCGN3230. The present invention describes a recombinant DNA
CC construct comprising a DNA sequence encoding a plant Delta-9 desaturase
CC protein. The present invention also provides a method of modifying fatty
CC acid composition in a host plant cell from a given fatty acid saturation
CC to a different fatty acid saturation, comprising growing a host plant
CC cell containing a recombinant DNA sequence which encodes a plant
CC desaturase under the control of regulatory elements functional in the
CC plant cell during lipid accumulation. Also, oilseeds having a modified
CC level of fatty acid saturation and oils produced from such oilseeds.
XX
XX Sequence 396 AA:
SQ
Query Match 72.3%; Score 1490; DB 19; Length 396;
Best Local Similarity 71.1%; Pred. No. 1.7e-134;
Matches 286; Conservative 50; Mismatches 52; Indels 14; Gaps 5;
OY 1 MALKLN-FOCKKNHPAFAKSPLEVRVSSP-RVFMASTVNSNSMVLNDLTKSP-----PN 53
DB 1 MALKLNFLSQTKLPSPALPMASTR--SPRFYASTLKSGSKVEVNLKPFMPREVN 58
OY 54 LOYTHSMPPQKLEIFKSLDDMARNNVLHLKSVKSWQPODYLPDPVSDGFEEQVREIRE 113
DB 59 VOYTHSMPPQKLEIFKSLDDMARNNVLHLKSVKSWQPODYLPDPVSDGFEEQVREIRE 118
OY 114 RAKEIPDDYFVVLVGMITEEALPTYMSMLNRCDDIKDETGAEPSSAMWTRAMTAENR 173
DB 119 RAKEIPDDYFVVLVGMITEEALPTYMSMLNRCDDIKDETGAEPSSAMWTRAMTAENR 178
OY 174 HGDLNKLKYLISGRVDMRKTEKTOYLIGSGMDIKSENSPYLGFIYTSFOERATFISHAN 233
DB 179 HGDLNKLKYLISGRVDMRKTEKTOYLIGSGMDIKSENSPYLGFIYTSFOERATFISHAN 238
OY 234 TAKLAOHYGDKNIAHIGSISASDERKHAATYKIVEKLAIEDPDTTVIAFADMMRKKTIM 293
DB 239 TARQAKHEGDKLQICGIIADDERKHAATYKIVEKLAIEDPDTTVIAFADMMRKKTIM 298
OY 294 PAHLMYDGSDELFEKHFHTAQAQRVXYASALDYCDILEFLVDKMWVERLTGLSDEGRAOE 353
DB 299 PAHLMYDGSDELFEKHFHTAQAQRVXYASALDYCDILEFLVDKMWVERLTGLSDEGRAOE 358
OY 354 YVCCELGPKTRVEEKVQGEKKKKAEP--VSFSWTFNRRLKI 394
DB 359 YVCCELGPKTRVEEKVQGEKKKKAEP--VSFSWTFNRRLKI 396
RESULT 3
AAR14189
ID AAR14189 standard; Protein; 396 AA.
XX
XX AAR14189:
XX
XX 11-DEC-1991 (first entry)
XX
XX R. communis delta9 desaturase from pCGN3230.
DE

```

XX Desaturase; fatty acid; saturation; chill tolerance; lipid;
KM herbicide.
XX Ricinus communis.
OS
PN MO9113972-A.
XX
PD 19-SEP-1991.
XX
PF 14-MAR-1991; 91WO-UO01746.
XX
PR 14-NOV-1990; 90US-0615784.
PR 16-MAR-1990; 90US-0494106.
PR 13-AUG-1990; 90US-0367373.
XX
PA (CALG-) CALGENE INC.
XX
PI Thompson G, Knauf V;
XX
DR WPI; 1991-295627/40.
DR N-PSDB; AAQ13964.
XX
PT DNA encoding a plant desaturase - used for modifying the satd.
PT fatty acid compsn. of plant cells and plant seeds
XX
PS Disclosure; Fig 3B; 128pp; English.
XX
CC Modification of fatty acid in a plant host cell to a different
CC percentage of fatty acid satn. is possible by growing a host plant
CC cell having integrated into its genome a recombinant DNA sequence
CC encoding this protein, under the control of regulatory elements
CC functional in the plant cell during lipid accumulation, under
CC conditions which will promote the activity of the regulatory elements.
CC By increasing the amt. of desaturase available in plant cells, an
CC increased percentage of unsatd. fatty acids may be provided, using
CC anti-sense technology, the amt. of desaturase can be decreased,
CC resulting in a higher percentage of fatty acids.
CC Using the desaturase gene and derivs. in cells and plants,
CC desirable traits such as chill tolerance may be introduced and
CC environmentally safe herbicide prods. may be provided.
CC See also AAQ13963-69.
XX
SQ Sequence 396 AA;
Query Match 71.8%; Score 1480; DB 12; Length 396;
Best local similarity 70.6%; Pred. No. 1.5e-133;
Matches 284; Conservative 51; Mismatches 53; Indels 14; Gaps 5;
OY 1 MALKLN-FÖCKKNHRAAKSPLEPTRVSSPRVMASTVNSMWLDNLKSP-----PN 53
DB 1 MALKNPFLSQTKLPSPALPPMASTR--SPKFYMASTLKSSEVENKKPFMPREYH 58
OY 54 LQVHSMSPQKLEIFKSLDDMRNNVLIHLKSVKSMQODILPPVSPDFEYRELRE 113
DB 59 VQVHSMSPQKLEIFKSLDDMRNNVLIHLKSVKSMQODILPPVSPDFEYRELRE 118
OY 114 RAKELIPDDYFVVLVGDMTTEALPTVMSMLNRCDSIKDETGAEPSSAMAMTAWTAENR 173
DB 119 RAKELIPDDYFVVLVGDMTTEALPTVMSMLNRCDSIKDETGAEPSSAMAMTAWTAENR 178
OY 174 HGDLLNKLYLSGRVDMRKIEKTIQYLLIGSGMDIKSENSPYLGFITYTSFOERATPISHAN 233
DB 179 HGDLLNKLYLSGRVDMRKIEKTIQYLLIGSGMDIKSENSPYLGFITYTSFOERATPISHAN 236
OY 234 TAKLAQHQNDNLNHHIGSISDEKRHATYATYKIVEXIAETIDPDVTYIAFADMMRKIKM 293
DB 239 TAKQAKHGDKLKLADICGTLADDEKRHEATYATYKIVEXIAETIDPDVTYIAFADMMRKIKM 298
OY 294 PAHLMTYDGSDELLFKHTAVAVQRYVYSALDYCDLLEFLVDKMWNERLGLSGDEGRKAOE 353
DB 299 PAHLMTYDGRDNLFDHFSVAVQRYVYSALDYCDLLEFLVDKMWNERLGLSGDEGRKAOE 358

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OY 354 YVCELGPKTRVEEKVQKREKKKAEHP-VSPSWIFNREIKI 394
DB 359 YVCELRPPRIRLQERAOGRK----EAPTPFSPWIFPDQVKL 396
RESULT 4
AAB48199
ID AAB48199 standard; Protein; 363 AA.
XX
AC AAB48199;
XX
DT 02-APR-2001 (first entry)
XX
DE Mature castor enzyme.
XX
KM Castor; delta9-18:0-acyl carrier protein desaturase; ACP; enzyme;
KM vegetable oil; fatty acid; nutrition; plant oil; mutant.
XX
OS Ricinus communis.
XX
FH Key Location/Qualifiers
FH FT Misc-difference 114
FH FT /note= "can be substituted by Ala"
FH FT Misc-difference 117
FH FT /note= "can be substituted by Arg"
FH FT Misc-difference 118
FH FT /note= "can be substituted by Gly"
FH FT Misc-difference 179
FH FT /note= "can be substituted by Val"
FH FT Misc-difference 181
FH FT /note= "can be substituted by Val"
FH FT Misc-difference 188
FH FT /note= "can be substituted by Leu"
PD MO200075170-A1.
PD 14-DEC-2000.
PF 08-JUN-2000; 2000MO-US15741.
PF 09-JUN-1999; 99US-0328550.
PR (BROO-) BROOKHAVEN SCI ASSOC LLC.
PA Shanklin J;
XX
PI WPI; 2001-091202/10.
DR N-PSDB; AAC84531.
XX
PT New mutant castor Delta9-18:0-Acyl Carrier Protein desaturase, useful
PT in producing commercially valuable products, e.g. vegetable oils useful
PT in human nutrition or as industrial chemicals
XX
PS Examples; Fig 1; 53pp; English.
XX
CC The invention relates to a new mutant castor Delta9-18:0-acyl carrier
CC protein (ACP) desaturase that has one or more amino acid substitutions
CC selected from: (a) Ala for Met at residue 114; (b) Arg for Thr at residue
CC 117; (c) Gly for Leu at residue 118; (d) Val for Pro at residue 179; (e)
CC Val for Thr at residue 181; (f) Leu for Gly at residue 186; and (g) Phe
CC for Thr at residue 181. The mutant castor Delta9-18:0-ACP desaturase is
CC useful in producing commercially useful products, such as vegetable oils
CC rich in monounsaturated fatty acids. Such vegetable oils are important in
CC human nutrition and can be used as renewable sources of industrial
CC chemicals. A method for specifically altering a function of a protein
CC through directed mutagenesis is also provided. The method can be used
CC altering enzymatic functions, binding functions or structural functions
CC of the castor desaturase enzyme. The method is also useful for
CC manipulating the physical properties and commercial uses of conventional
CC plant oils. The present sequence represents the mature castor enzyme.
XX
SQ Sequence 363 AA;

```


Db 297 SMFAHLMYDGRDNLPEHPSAVAQRLGVYAKDYADILLEFLVGKMYADLTLGLSGEGRKA 356
 Oy 352 QEYVCELGPRIKIRVEEKVKQEKKKAEHP-VSEFSWTFNRELKI 394
 Db 357 ODYVCGLPRIKIRRLERRAQGRK-----EGPVVPSWTFNFDQVKL 396
 RESULT 8
 AAR22048
 ID AAR22048 standard; Protein; 396 AA.
 AC AAR22048;
 XX 07-JUL-1992 (first entry)
 DT Carthamus tinctorius desaturase.
 DE Carthamus tinctorius desaturase.
 KM Safflower; fatty acid synthesis; seed; acyl carrier protein;
 KW lipids.
 OS Carthamus tinctorius.
 PN W09203564-A.
 XX 05-MAR-1992.
 PD 15-AUG-1991; 91WO-0005801.
 PF 26-JUN-1991; 91US-0721761.
 PR 15-AUG-1990; 90US-0568493.
 PA (CALG-) CALGENE INC.
 PI Knauf VC, Thompson GA;
 XX WPI: 1992-096907/12.
 DR N-PSDB: A0022616.
 XX New plant beta-keto:acyl synthase protein - obtd. from Ricinus
 PT communis, useful e.g. for modifying fatty acid compn.
 PS Disclosure; Fig 8; 157pp; English.
 CC The protein sequence was deduced from the desaturase gene isolated
 CC from Carthamus tinctorius as the clone pCGN2754. The clone can be
 CC used to construct acyl carrier protein expression cassettes in a
 CC binary vector for plant transformation. This allows integration
 CC of nucleic acids encoding a desaturase sequence and a synthase
 CC sequence into the genome of a host cell. A plant desaturase
 CC includes any enzyme capable of catalysing the insertion of a first
 CC double bond into a fatty acid-ACP moiety especially between C9-C10.
 CC See also AAR22046-53.
 SO Sequence 396 AA;
 Query Match 68.2%; Score 1406; DB 13; Length 396;
 Best Local Similarity 67.1%; Pred. No. 2e-126;
 Matches 271; Conservative 54; Mismatches 61; Indels 18; Gaps
 Oy 1 MALKI---NFOCKKHRAFAKSPIDPVTVSSPRVFMASTVNSNMVLDNLKSP----- 51
 Db 1 MALKTPVTLTOSERKRSFSPKK---ANLRSPKPRAMASTLSSSPKVDNAKPPQPPRE 56
 Oy 52 PNLQVTHSPPOKLEIFKSLDDMARNNVLIHLKSYEKSMQPDQYLPDPVSDGFEEQVRL 111
 Db 57 VHVQVTHSPPOKLEIFKSLDGMAQNLIVHLKPYEKKQAOQDFLPDPVSEGFDEQVKL 116
 Oy 112 RERAKELPDDYFVVLVGDMTTEALPTYSMLNRCDGIKDETGAPPSAWAMTRAWTAEE 171
 Db 117 RARAKELPDDYFVVLVGDMTTEALPTYSMLNLTLDGVREDGASLTPKAVVTRAWTAEE 176
 Oy 172 NRHDDLNLKTYILSGRVDMAKIEKTIQYLTJSSGMDIKESNSPYLGFITYTSFOERATFISH 231

[illegible]


```

XX 11-DEC-1991 (first entry)
XX B. campestris delta9 desaturase from PCGN3235.
XX Desaturase; fatty acid; saturation; chill tolerance; lipid;
XX herbicide.
XX Brassica campestris.
XX MO9113972-A.
XX 19-SEP-1991.
XX 14-MAR-1991; 91WO-0001746.
XX 14-NOV-1990; 90US-0615784.
XX 16-MAR-1990; 90US-0494106.
XX 13-AUG-1990; 90US-0567373.
XX (CALG-) CALGENE INC.
XX Thompson G, Knaut V;
XX WPI: 1991-295627/40.
XX N-PSDB: AAQ13965.
XX DNA encoding a plant desaturase - used for modifying the satd.
XX fatty acid compsn. of plant cells and plant seeds
XX Disclosure: Fig 4C; 128bp; English.
XX Modification of fatty acid in a plant host cell to a different
XX percentage of fatty acid satn. is possible by growing a host plant
XX cell having integrated into its genome a recombinant DNA sequence
XX encoding this protein, under the control of regulatory elements
XX functional in the plant cell during lipid accumulation, under
XX conditions which will promote the activity of the regulatory elements.
XX By increasing the amt. of desaturase available in plant cells, an
XX increased percentage of unsatd. fatty acids may be provided, using
XX anti-sense technology, the amt. of desaturase can be decreased,
XX resulting in a higher percentage of fatty acids.
XX Using the desaturase gene and derivs. in cells and plants,
XX desirable traits such as chill tolerance may be introduced and
XX environmentally safe herbicide prods. may be provided.
XX See also AAQ13963-69.
XX
SQ Sequence 398 AA:
Query Match 67.7%; Score 1396; DB 12; Length 398;
Best Local Similarity 66.9%; Pred. NO. 1.8e-125;
Matches 269; Conservative 55; Mismatches 66; Indels 12; Gaps 4;
QY 1 MALKLNFOCKR--NHPAFAKSPPLVTRVSSPRVEMASTVNSNVLNLSKSP-----P 52
    ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1 MALKLNPLASOPYNPPSS-ARPPITFRSPKFLCLASSSPALSSKEVESLKKFPPTPKREV 59
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 53 NLOVTHSMPPOKLEIFKSLDDMARNNVLIHLKSVESKMQPODYLPDPVSDGFEEQVREL 112
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 60 HVOYLHSHMPPOKLEIFKSLDDMARNNVLIHLKSVESKMQPODYLPDPVSDGFEEQVREL 119
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 113 ERAKEIPDDYFVVLVGMITEALPTYSMLNRCDSIKDETGAEPSAMAMTAWTAEN 172
    |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 120 ERARLPPDYFVVLVGMITEALPTYSMLNRCDSIKDETGAEPSAMAMTAWTAEN 179
    |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 173 RHGDLNLTLYISGVNDAKRIKTIQYLLIGSGMDIKSESPYIGTYTSFOERATFISHA 232
    |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 180 RHGDLNLTLYISGVNDAKRIKTIQYLLIGSGMDIKSESPYIGTYTSFOERATFISHG 239
    |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 233 NTAKLAOHYGDKNLHIGSGIASDEKRNATATYTKIYELAIEDPDTTYVAFAMMRKITF 292
    |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 240 NTARAKHEGDLKLOIGCTIAADEKRHETATYTKIYELFEIDPDCTVMAFAMMRKITIS 299
    |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

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QY 293 MPAHLMTDGSEDLLEFKHETAVAOXVYXSALDYCDILEFVLVDKMNVERLTGSDGKRAQ 352
    ||||| :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 300 MPAHLMYDGRSELEFDNFSSVAQRLGYTAKDYADILEFVGRWKIESLTGLSGGNKAQ 359
    |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 353 EYVCELGPKIRRVKEKVGKKEKKAEHPVSESMFNRELKI 394
    |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 360 EYLCGLPRIRLRIDERAQARAKGP--KVPFSWIHREVOL 398
    |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

RESULT 14
AAW14798
ID AAW14798 standard; Protein; 398 AA.
XX
AC AAW14798;
XX
DB 03-JUL-1997 (first entry)
XX
DE Rapeseed stearyl-ACP desaturase BMD9.
XX
KM Stearoyl-ACP desaturase; rapeseed; acyl-ACP thioesterase;
KM antisenase; triglyceride; stearic acid; transgenic plant; oilseed;
KM vegetable oil; mangosteen; Garcinia mangifera.
XX
OS Brassica napus cv. 212/86.
XX
PN MO9712047-A1.
XX
PD 03-APR-1997.
XX
PE 30-SEP-1996; 96WO-US16078.
XX
PR 29-SEP-1995; 95US-0537083.
XX
PA (CALG ) CALGENE INC.
XX
PI Knaut VC, Kridl J, Lassner MW;
XX
DR WPI: 1997-212906/19.
XX
DB N-PSDB: AAT63438.
XX
PT Increasing levels of stearate in plant seed triglyceride(s) -
PT using a DNA sequence encoding acyl-ACP thioesterase protein having
PT substantial activity on C18:0 acyl-ACP substrates
XX
PS Example 5; Fig7A-7C; 55bp; English.
XX
CC Oilseed rape stearyl-ACP desaturases BMD11 (AAW14797) and BMD9
CC (AAW14798) each catalyze the desaturation of stearyl-ACP (C18:0) to
CC oleoyl-ACP (C18:1). Their amino acid sequences were deduced from
CC cDNA clones (AAT63437-38) isolated from a Brassica napus cv. 212/86
CC mid-turation seed cDNA library. An antisenase gene was constructed
CC to generate antisenase RNA homologous to both BMD9 and BMD11. In
CC transgenic Brassica plants expressing the stearyl-ACP desaturase
CC antisenase construct and mangosteen Class I acyl-ACP thioesterase
CC GammaPal (see also AAW14795), levels of C18:0 in the seed oil may
CC exceed 50% of total fatty acids.
XX
SQ Sequence 398 AA:
Query Match 67.7%; Score 1396; DB 18; Length 398;
Best Local Similarity 66.9%; Pred. NO. 1.8e-125;
Matches 269; Conservative 55; Mismatches 66; Indels 12; Gaps 4;
QY 1 MALKLNFOCKRNHPAARAKSPPLVTRVSSPR--VFMASTVNSNVLNLSKSP-----P 52
    ||||| :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 1 MALKLNPLASOPYNPPSSAR-PVSTFRSPKFLCLASSSPALSSKEVESLKKFPPTPKREV 59
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 53 NLOVTHSMPPOKLEIFKSLDDMARNNVLIHLKSVESKMQPODYLPDPVSDGFEEQVREL 112
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 60 HVOYLHSHMPPOKLEIFKSLDDMARNNVLIHLKSVESKMQPODYLPDPVSDGFEEQVREL 119
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 113 ERAKEIPDDYFVVLVGMITEALPTYSMLNRCDSIKDETGAEPSAMAMTAWTAEN 172
    |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

```

Db 120 ERARELPDVFVVLVGDMTTEALPTVQTMNLTDGVRDEFGASPTSWAIVTAWTAEN 179
 QY 173 RHGDLNKKYLYLSGRVDMRKIEKTIQYLLGSGMDIKSENSPYLFTYTSFOERATFISHA 232
 Db 180 RHGDLNKKYLYLSGRVDMRKIEKTIQYLLGSGMDIKSENSPYLFTYTSFOERATFISHG 239
 QY 233 NTKAKLAHQYGDKNLAHICGSIASDEKRRHATATYTKIVEKLAIEDPTTVIAFADMMRKIT 292
 Db 240 NTKAKLAHQYGDKNLAHICGSIASDEKRRHATATYTKIVEKLAIEDPTTVIAFADMMRKIS 299
 QY 293 MPAHLWYDGSDELLFKHFTAVAQRYVXSALDYCDILEFLYDKMNVRELTLGSDGGRKAO 352
 Db 300 MPAHLWYDGRDESLFDNFSVAQRIGVYATKADYADILEFLVGRWKIESLTGLSGGNKAO 359
 QY 353 EYVCELGPKTRVVEEKVQGEKKKKAHPVSFSWIFNRELKI 394
 Db 360 EYICGLTPRIRRLDERAQAARKGP---KVPSWIHREVQL 398

RESULT 15

AAW4351 standard; Protein: 398 AA.

AAW4351:

28-MAY-1998 (first entry)

Brassica campestris desaturase from clone pCGN3235.

Brassica campestris; castor bean; delta-9 desaturase; oilseed;

fatty acid saturation.

Brassica campestris.

US5723595-A.

03-MAR-1998.

06-JUN-1995; 95US-0471791.

16-SEP-1991; 91US-0762762.

16-MAR-1990; 90US-0494106.

13-AUG-1990; 90US-0567373.

14-NOV-1990; 90US-0615784.

14-MAR-1991; 91WO-US01746.

06-JUN-1995; 95US-0471791.

(CALJ) CALGENE INC.

Knauf VC, Thompson GA;

MP1: 1998-178544/16.

N-PSDB; AAV15253.

Claim 9: Column 63-66; 87pp; English.

The present sequence represents a Brassica campestris desaturase from clone pCGN3235. The present invention describes a recombinant DNA construct comprising a DNA sequence encoding a plant Delta-9 desaturase protein. The present invention also provides a method of modifying fatty acid composition in a host plant cell from a given fatty acid saturation to a different fatty acid saturation, comprising growing a host plant cell containing a recombinant DNA sequence which encodes a plant desaturase under the control of regulatory elements functional in the plant cell during lipid accumulation. Also, oilseeds having a modified level of fatty acid saturation and oils produced from such oilseeds.

Sequence 398 AA:

Query Match 67.7%; Score 1396; DB 19; Length 398;
 Best Local Similarity 66.9%; Pred. No. 1.8e-125;
 Matches 269; Conservative 55; Mismatches 66; Indels 12; Gaps 4;

QY 1 MALKLNFQCKR--NHPAFAKSPPLVTRVSSPRVEMASTVNSNSWLDMLKSP-----P 52
 Db 1 MALKLNPASQYNNPSS-ARPPISITFRSPKFLCLASSPALSKEVESLKKPFTPPREY 59
 QY 53 NIQVTHSNPPOKLETFKSLDDMARNNVLIHLKSVESKMPQDYLDPDVSDFGEQYREL 112
 Db 60 HVOVLSMPPOKLETFKSMEDMABQMLYQLDVKSQWQPODFLPDASDGFEDQYREL 119
 QY 113 ERAKEIPDDVFVVLVGDMTTEALPTVSMNLNRCGDIKDETGAEPSAAMWTAEN 172
 Db 120 ERARELPDVFVVLVGDMTTEALPTVQTMNLTDGVRDEFGASPTSWAIVTAWTAEN 179
 QY 173 RHGDLNKKYLYLSGRVDMRKIEKTIQYLLGSGMDIKSENSPYLFTYTSFOERATFISHA 232
 Db 180 RHGDLNKKYLYLSGRVDMRKIEKTIQYLLGSGMDIKSENSPYLFTYTSFOERATFISHG 239
 QY 233 NTKAKLAHQYGDKNLAHICGSIASDEKRRHATATYTKIVEKLAIEDPTTVIAFADMMRKIT 292
 Db 240 NTKAKLAHQYGDKNLAHICGSIASDEKRRHATATYTKIVEKLAIEDPTTVIAFADMMRKIS 299
 QY 293 MPAHLWYDGSDELLFKHFTAVAQRYVXSALDYCDILEFLYDKMNVRELTLGSDGGRKAO 352
 Db 300 MPAHLWYDGRDESLFDNFSVAQRIGVYATKADYADILEFLVGRWKIESLTGLSGGNKAO 359
 QY 353 EYVCELGPKTRVVEEKVQGEKKKKAHPVSFSWIFNRELKI 394
 Db 360 EYICGLTPRIRRLDERAQAARKGP---KVPSWIHREVQL 398

Search completed: December 1, 2002, 21:20:14
 Job time : 41 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 1, 2002, 21:19:11 ; Search time 21 Seconds

(Without alignments)
1803.665 Million cell updates/sec

Title: US-09-732-597-2

Perfect score: 2062
Sequence: 1 MALKNFQCKKNHPAFAKS.....KKKAHPVSFWIFNRELKI 394

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1545.5	75.0	385	2 A47245	acyl-[acyl-carrier
2	1490	72.3	396	1 OHCSAD	acyl-[acyl-carrier
3	1422.5	69.0	411	2 T07806	acyl-[acyl-carrier
4	1410.5	68.4	399	1 OHSPAD	acyl-[acyl-carrier
5	1408	68.3	396	2 B39170	acyl-[acyl-carrier
6	1406	68.2	396	2 A39173	acyl-[acyl-carrier
7	1396	67.7	398	2 S23351	acyl-[acyl-carrier
8	1395	67.7	396	2 T14264	acyl-[acyl-carrier
9	1386.5	67.2	393	2 S44202	acyl-[acyl-carrier
10	1386.5	67.2	399	2 S24955	acyl-[acyl-carrier
11	1385.5	67.0	401	2 T07653	acyl-[acyl-carrier
12	1381.5	67.0	401	2 E84869	stearyl-ACP desat
13	1381	67.0	396	2 T14268	acyl-[acyl-carrier
14	1375.5	66.7	397	2 T10793	acyl-[acyl-carrier
15	1352	65.6	396	2 T14172	acyl-[acyl-carrier
16	1347.5	65.3	407	2 S71262	acyl-[acyl-carrier
17	1320.5	64.0	394	2 T51494	stearyl-acyl carr
18	1310.5	63.6	390	2 T04097	acyl-[acyl-carrier
19	1246	60.4	396	2 S31959	acyl-[acyl-carrier
20	1223.5	59.3	401	2 T51493	stearyl-acyl carr
21	1197	58.1	374	2 A96502	probable acyl-acyl
22	295	14.3	328	2 T35035	probable acyl-acyl
23	271.5	13.2	338	2 D87182	acyl-[ACP] desatur
24	256.5	12.4	338	2 H70810	probable desat pro
25	135	6.5	275	2 C87153	acyl-[ACP] desatur
26	122.5	5.9	2269	2 T28677	rhodity protein -
27	121.5	5.9	275	2 D70896	probable desat pro
28	114.5	5.6	1557	2 T18412	lipid-binding prot
29	108	5.2	616	2 A64341	hypothetical prote

30	105.5	5.1	393	2 C71836	tryptophan synthas
31	105.5	5.1	520	2 P90596	restriction-modifi
32	105.5	5.1	520	2 A99566	restriction-modifi
33	105.5	5.1	684	2 AE2004	hypothetical prote
34	104.5	5.1	524	2 T43050	cyclin E - Caenorh
35	104.5	5.1	570	2 T30156	hypothetical prote
36	103	5.0	244	2 C89811	hypothetical prote
37	102.5	5.0	393	2 F64679	tryptophan synthas
38	102.5	5.0	520	2 S49395	HsdM1 protein - My
39	101.5	4.9	846	2 JC7720	acetyltransferase
40	100.5	4.9	1027	2 T46296	hypothetical prote
41	100.5	4.9	3643	2 T36410	probable polyketid
42	100	4.8	604	2 T19682	hypothetical prote
43	99.5	4.8	517	2 T48283	ankyrin-like prote
44	99.5	4.8	1120	2 JC7765	mitotic spindle as
45	99	4.8	782	2 A82940	hypothetical prote

ALIGNMENTS

RESULT 1

A47245
acyl-[acyl-carrier-protein] desaturase (EC 1.14.19.2) - coriander
N:Alternate names: type II acyl-ACP desaturase
C:Species: Coriandrum sativum (coriander)
C>Date: 21-Jan-1994 #sequence_rev18-Nov-1994 #text_change 03-Jun-2002
C:Accession: A47245
R:Caenor, E.B.; Shanklin, J.; Ohlrogge, J.B.
Proc. Natl. Acad. Sci. U.S.A. 89, 11184-11188, 1992
A:Title: Expression of a coriander desaturase results in petroselinic acid*production
A:Reference number: A47245; M0ID:93087491; PMID:1454797
A:Accession: A47245
A>Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-385 <CAH>
A:Cross-references: GB:M93115; MID:g167388; PIDN:ANC63059.1; PID:g167389
A:Note: sequence extracted from NCBI backbone (NCBI:119750, NCBI:P:119751)
C:Superfamily: acyl-[acyl-carrier-protein] desaturase
C:Keywords: chloroplast; oxidoreductase

Query Match	75.0%	Score 1545.5;	DB 2;	Length 385;
Best local Similarity	73.1%	Pred. No. 2.6e-105;		
Matches 296;	Conservative 42;	Mismatches 36;	Indels 31;	Gaps 5;
QY	1 MALKNFQCKKNHPAFAKSPLPTRVSSP-----RVMASVNSNSVLDNLK 49			
DB	1 MALKNLMTLQCKRN-----MFTRIAPQAGRVRKSVMASTLHASPVEFKL 51			
QY	50 SPNLIQVTHSMPOKLEIFKSLDDMARNVLIHLKSVKSNQPODYLPPVSDGEEOVR 109			
DB	52 AG-----RPEVDLFLNSLBGMARDNLIHLKSVNSNQPODYLPPVSDAFEDQVK 102			
QY	110 ELBRKAEIPDDYFVLVGMITEBALPTYMSMNRCDGIDEGAEFSANAMTRANTA 169			
DB	103 EMERKADIDDEYFVVLVGMITEBALPTYMSMNRCDGIDEGAEFSANAMTRANTA 162			
QY	170 EENRHGDLNKKYTLVLSGRVVRKTEKTYOVLIGSGMDIKSNPSPLGRTYVSPORAFPI 229			
DB	163 EENRHGDLNKKYTLVLSGRVVRKTEKTYOVLIGSGMDIKSNPSPLGRTYVSPORAFPI 222			
QY	230 SHANTAKLAOHYGDKNLAHICGSIASDEKRAHTAYTKIVERLAIEDPPTVYIAFADMRK 289			
DB	223 SHANTAKLAOHYGDKNLAHICGSIASDEKRAHTAYTKIVERLAIEDPPTVYIAFADMRK 282			
QY	290 KITPAHLMTDGSDELLFKHFTAVARXYXSALDYCDILEFLVDKMWVERLTGSDGR 349			
DB	283 KITPAHLMTDGSDELLFKHFTAVARXYXSALDYCDILEFLVDKMWVERLTGSDGR 342			
QY	350 KAOEYVCGLPKIRVVEKVGKREKKKKAHPVPSWFNRELKI 394			
DB	343 KAOEYVCGLPKIRVVEKVGKREKKKKAHPVPSWFNRELKI 385			

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